

XX ABT35053;
 XX 12-JUN-2003 (first entry)
 XX Tumour suppression related human fukutin oligo SEQ ID No 690.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 XX schizophrenia; protein chip; gene therapy; tumour suppression;
 XX human fukutin; ds.
 XX Homo sapiens.
 XX WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB04208.
 XX 17-SEP-2001; 2001FR-0011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Anson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX New isolated nucleic acid, useful for treating viral diseases
 XX associated with tumors and cell degeneration, also related
 XX polypeptides, antibodies and transfected cells -
 XX Disclosure; Page 114; 720pp; French.
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 XX given in the specification, a sequence containing at least 15
 XX consecutive nucleotides from the 17 mer sequence, a sequence with, after
 XX optimal alignment, at least 80 % identity to the 17 mer sequence, a
 XX sequence that hybridizes to them under highly stringent conditions, or
 XX the complement of any of them, or the corresponding RNA. The novel
 XX isolated nucleic acids of the invention are useful as probes and primers
 XX for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 XX e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 XX and for production of recombinant polypeptides. Any of the nucleic acids,
 XX polypeptides, vectors containing the nucleic acids, cells containing the
 XX vector or antibodies directed against the polypeptides are useful for
 XX preparation of pharmaceuticals for prevention and/or treatment of viral
 XX diseases that are characterised by development of tumours or cell
 XX degeneration, specifically cancer but also Alzheimer's disease and
 XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 XX patient samples is useful for diagnosis and/or prognosis of these
 XX diseases. The polypeptides can also be used to generate antibodies, and
 XX both the polypeptide and antibodies are useful as components of protein
 XX chips. The nucleic acid sequences of the invention can be used in gene
 XX therapy. This polynucleotide sequence represents a tumour suppression
 XX related human fukutin oligonucleotide of the invention.

Sequence 17 BP; 5 A; 3 C; 3 G; 6 T; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 566 ATGAATATCCAGAAC 581
 |||||
 16 ATGAATGTCGATC 1

SULT 568
 T35977
 ABT35977 standard; DNA; 17 BP.
 ABT35977;

XX 12-JUN-2003 (first entry)
 XX Tumour suppression related human fukutin oligo SEQ ID No 1614.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 XX schizophrenia; protein chip; gene therapy; tumour suppression;
 XX human fukutin; ds.
 XX Homo sapiens.
 XX WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB04208.
 XX 17-SEP-2001; 2001FR-0011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Anson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX New isolated nucleic acid, useful for treating viral diseases
 XX associated with tumors and cell degeneration, also related
 XX polypeptides, antibodies and transfected cells -
 XX Disclosure; Page 221; 720pp; French.
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 XX given in the specification, a sequence containing at least 15
 XX consecutive nucleotides from the 17 mer sequence, a sequence with, after
 XX optimal alignment, at least 80 % identity to the 17 mer sequence, a
 XX sequence that hybridizes to them under highly stringent conditions, or
 XX the complement of any of them, or the corresponding RNA. The novel
 XX isolated nucleic acids of the invention are useful as probes and primers
 XX for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 XX e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 XX and for production of recombinant polypeptides. Any of the nucleic acids,
 XX polypeptides, vectors containing the nucleic acids, cells containing the
 XX vector or antibodies directed against the polypeptides are useful for
 XX preparation of pharmaceuticals for prevention and/or treatment of viral
 XX diseases that are characterised by development of tumours or cell
 XX degeneration, specifically cancer but also Alzheimer's disease and
 XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 XX patient samples is useful for diagnosis and/or prognosis of these
 XX diseases. The polypeptides can also be used to generate antibodies, and
 XX both the polypeptide and antibodies are useful as components of protein
 XX chips. The nucleic acid sequences of the invention can be used in gene
 XX therapy. This polynucleotide sequence represents a tumour suppression
 XX related human fukutin oligonucleotide of the invention.

Sequence 17 BP; 9 A; 2 C; 1 G; 5 T; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 999 ATCATAACATATAATTA 1014
 |||||
 2 ATCATAAATACATTA 17

RESULT 569
 ABT36351/C
 ID ABT36351 standard; DNA; 17 BP.
 XX ABT36351;
 XX ABT36351;
 DT 12-JUN-2003 (first entry)

XX DE Tumour suppression related human fukutin oligo SEQ ID No 1988.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrénia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
XX Homo sapiens.
OS
XX WO2003025175-A2.
PN
XX 27-MAR-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB04208.
XX
XX 17-SEP-2001; 2001FR-0011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases
PT associated with tumors and cell degeneration, also related
PT polypeptides, antibodies and transfected cells -
PT
XX Disclosure; Page 265; 720pp; French.
PS
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15
CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
CC sequence that hybridizes to them under highly stringent conditions, or
CC the complement of any of them, or the corresponding RNA. The novel
CC isolated nucleic acids of the invention are useful as probes and primers
CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
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CC and for production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrénia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention.
XX
XX Sequence 17 BP; 5 A; 2 C; 4 G; 6 T; 0 other;
SQ
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1462 TTATGTACACATAGAT 1477
DB 17 TTATGTACACAGAT 2
RESULT 570
ABT36416/C
ID ABT36416 standard; DNA; 17 BP.
AC ABT36416;
XX
XX 12-JUN-2003 (first entry)
DT
XX Tumour suppression related human fukutin oligo SEQ ID No 2053.
DE

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrénia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
XX Homo sapiens.
OS
XX WO2003025175-A2.
PN
XX 27-MAR-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB04208.
XX
XX 17-SEP-2001; 2001FR-0011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases
PT associated with tumors and cell degeneration, also related
PT polypeptides, antibodies and transfected cells -
PT
XX Disclosure; Page 273; 720pp; French.
PS
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15
CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
CC sequence that hybridizes to them under highly stringent conditions, or
CC the complement of any of them, or the corresponding RNA. The novel
CC isolated nucleic acids of the invention are useful as probes and primers
CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
CC and for production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrénia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention.
XX
XX Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 other;
SQ
Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 744 TTTGCTAGATGTGAT 759
DB 17 TATGCTACATGTGAT 2
RESULT 571
ABT37756
ID ABT37756 standard; DNA; 17 BP.
AC ABT37756;
XX
XX 12-JUN-2003 (first entry)
DT
XX Tumour suppression related human fukutin oligo SEQ ID No 3393.
DE
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW

antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
schizophrenia; protein chip; gene therapy; tumour suppression;
human fukutin; ds.

Homo sapiens.

WO2003025175-A2.

27-MAR-2003.

17-SEP-2002; 2002WO-IB04208.

17-SEP-2001; 2001FR-0011978.

(MOLE-) MOLECULAR ENGINES LAB.

Telerman A, Amson R, Tuijnder M;

WPI; 2003-313353/30.

New isolated nucleic acid, useful for treating viral diseases
associated with tumors and cell degeneration, also related
polypeptides, antibodies and transfected cells -

Disclosure; Page 430; 720pp; French.

The invention relates to a novel isolated 17 mer nucleic acid sequence,
given in the specification, a sequence containing at least 15
consecutive nucleotides from the 17 mer sequence, a sequence with, after
optimal alignment, at least 80 % identity to the 17 mer sequence, a
sequence that hybridizes to them under highly stringent conditions, or
the complement of any of them, or the corresponding RNA. The novel
isolated nucleic acids of the invention are useful as probes and primers
for detecting, identifying, quantifying and/or amplifying a nucleic acid,
e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
and for production of recombinant polypeptides. Any of the nucleic acids,
polypeptides, vectors containing the nucleic acids, cells containing the
vector or antibodies directed against the polypeptides are useful for
preparation of pharmaceuticals for prevention and/or treatment of viral
diseases that are characterised by development of tumours or cell
degeneration, specifically cancer but also Alzheimer's disease and
schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
patient samples is useful for diagnosis and/or prognosis of these
diseases. The polypeptides can also be used to generate antibodies, and
both the polypeptide and antibodies are useful as components of protein
chips. The nucleic acid sequences of the invention can be used in gene
therapy. This polynucleotide sequence represents a tumour suppression
related human fukutin oligonucleotide of the invention.

Sequence 17 BP; 9 A; 3 C; 2 G; 3 T; 0 other;

Query Match 1.0%; Score 12.9; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

769 ATCATATAAAATGAT 784

2 ATCATATAAACAGT 17

SULT 572

T38062

ABT38062 standard; DNA; 17 BP.

ABT38062;

12-JUN-2003 (first entry)

Tumour suppression related human fukutin oligo SEQ ID No 3699.

Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
schizophrenia; protein chip; gene therapy; tumour suppression;

KW human fukutin; ds.

XX Homo sapiens.

PN WO2003025175-A2.

XX 27-MAR-2003.

PP 17-SEP-2002; 2002WO-IB04208.

PR 17-SEP-2001; 2001FR-0011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases
associated with tumors and cell degeneration, also related
polypeptides, antibodies and transfected cells -

PS Disclosure; Page 466; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
given in the specification, a sequence containing at least 15
consecutive nucleotides from the 17 mer sequence, a sequence with, after
optimal alignment, at least 80 % identity to the 17 mer sequence, a
sequence that hybridizes to them under highly stringent conditions, or
the complement of any of them, or the corresponding RNA. The novel
isolated nucleic acids of the invention are useful as probes and primers
for detecting, identifying, quantifying and/or amplifying a nucleic acid,
e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
and for production of recombinant polypeptides. Any of the nucleic acids,
polypeptides, vectors containing the nucleic acids, cells containing the
vector or antibodies directed against the polypeptides are useful for
preparation of pharmaceuticals for prevention and/or treatment of viral
diseases that are characterised by development of tumours or cell
degeneration, specifically cancer but also Alzheimer's disease and
schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
patient samples is useful for diagnosis and/or prognosis of these
diseases. The polypeptides can also be used to generate antibodies, and
both the polypeptide and antibodies are useful as components of protein
chips. The nucleic acid sequences of the invention can be used in gene
therapy. This polynucleotide sequence represents a tumour suppression
related human fukutin oligonucleotide of the invention.

XX Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 573 ATCCAGAACATCTTAA 588

Db 2 ATCCAGAGATCTAA 17

RESULT 573

ABT38413/C

ID ABT38413 standard; DNA; 17 BP.

XX ABT38413;

XX 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 4050.

Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
schizophrenia; protein chip; gene therapy; tumour suppression;
human fukutin; ds.

OS Homo sapiens.
 XX WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB04208.
 XX 17-SEP-2001; 2001FR-0011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Tellerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX New isolated nucleic acid, useful for treating viral diseases
 XX associated with tumors and cell degeneration, also related
 XX polypeptides, antibodies and transfected cells -
 XX Disclosure; Page 507; 720pp; French.
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 XX given in the specification, a sequence containing at least 15
 XX consecutive nucleotides from the 17 mer sequence, a sequence with, after
 XX optimal alignment, at least 80 % identity to the 17 mer sequence, a
 XX sequence that hybridizes to them under highly stringent conditions, or
 XX the complement of any of them, or the corresponding RNA. The novel
 XX isolated nucleic acids of the invention are useful as probes and primers
 XX for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 XX e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 XX and for production of recombinant polypeptides. Any of the nucleic acids,
 XX polypeptides, vectors containing the nucleic acids, cells containing the
 XX vector or antibodies directed against the polypeptides are useful for
 XX preparation of pharmaceuticals for prevention and/or treatment of viral
 XX diseases that are characterised by development of tumours or cell
 XX degeneration, specifically cancer but also Alzheimer's disease and
 XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 XX patient samples is useful for diagnosis and/or prognosis of these
 XX diseases. The polypeptides can also be used to generate antibodies, and
 XX both the polypeptide and antibodies are useful as components of protein
 XX chips. The nucleic acid sequences of the invention can be used in gene
 XX therapy. This polynucleotide sequence represents a tumour suppression
 XX related human fukutin oligonucleotide of the invention.

Y 1099 AGATGATCATGAT 1114
 |||||
 b 17 AAGTGAACATAGAT 2

RESULT 574
 BT39158/C
 D ABT39158 standard; DNA; 17 BP.
 X
 X ABT39158;
 X
 X 12-JUN-2003 (first entry)
 X
 X Tumour suppression related human fukutin oligo SEQ ID No 4795.
 X Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 W antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 W schizophrenia; protein chip; gene therapy; tumour suppression;
 W human fukutin; ds.
 X Homo sapiens.
 X
 X

PN WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB04208.
 XX 17-SEP-2001; 2001FR-0011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Tellerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX New isolated nucleic acid, useful for treating viral diseases
 XX associated with tumors and cell degeneration, also related
 XX polypeptides, antibodies and transfected cells -
 XX Disclosure; Page 594; 720pp; French.
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 XX given in the specification, a sequence containing at least 15
 XX consecutive nucleotides from the 17 mer sequence, a sequence with, after
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 XX sequence that hybridizes to them under highly stringent conditions, or
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 XX isolated nucleic acids of the invention are useful as probes and primers
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 XX vector or antibodies directed against the polypeptides are useful for
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 XX patient samples is useful for diagnosis and/or prognosis of these
 XX diseases. The polypeptides can also be used to generate antibodies, and
 XX both the polypeptide and antibodies are useful as components of protein
 XX chips. The nucleic acid sequences of the invention can be used in gene
 XX therapy. This polynucleotide sequence represents a tumour suppression
 XX related human fukutin oligonucleotide of the invention.

SQ Sequence 17 BP; 4 A; 3 C; 2 G; 8 T; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1608 GAAACATTTAAATAT 1623
 |||||
 Db 17 GGAACATTTAAAGAT 2

RESULT 575
 BT39376
 ID ABT39376 standard; DNA; 17 BP.
 XX
 XX AC ABT39376;
 XX
 XX 12-JUN-2003 (first entry)
 XX
 XX Tumour suppression related human fukutin oligo SEQ ID No 5013.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 W antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 W schizophrenia; protein chip; gene therapy; tumour suppression;
 W human fukutin; ds.
 X Homo sapiens.
 X
 X WO2003025175-A2.
 XX

D 27-MAR-2003.
 X 17-SEP-2002; 2002WO-IB04208.
 F 17-SEP-2001; 2001FR-0011978.
 R (MOLE-) MOLECULAR ENGINES LAB.
 X Telerman A, Anson R, Tuijnder M;
 X WPI; 2003-313353/30.
 X New isolated nucleic acid, useful for treating viral diseases
 X associated with tumors and cell degeneration, also related
 X polypeptides, antibodies and transfected cells -
 X Disclosure; Page 620; 720pp; French.
 X The invention relates to a novel isolated 17 mer nucleic acid sequence,
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 X vector or antibodies directed against the polypeptides are useful for
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 X diseases that are characterised by development of tumours or cell
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 X therapy. This polynucleotide sequence represents a tumour suppression
 X related human fukutin oligonucleotide of the invention.

Sequence 17 BP; 9 A; 4 C; 1 G; 3 T; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1243 ATTCAGATTAACAC 1258
 |||||
 2 ATTCAGATTAACAC 17

RESULT 576
 ABT39378
 ABT39378 standard; DNA; 17 BP.
 ABT39378;
 12-JUN-2003 (first entry)
 Tumour suppression related human fukutin oligo SEQ ID No 5015.
 Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 schizophrenia; protein chip; gene therapy; tumour suppression;
 human fukutin; ds.
 Homo sapiens.
 WO2003025175-A2.
 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB04208.
 XX 17-SEP-2001; 2001FR-0011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Anson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX New isolated nucleic acid, useful for treating viral diseases
 XX associated with tumors and cell degeneration, also related
 XX polypeptides, antibodies and transfected cells -
 XX Disclosure; Page 620; 720pp; French.
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
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 XX consecutive nucleotides from the 17 mer sequence, a sequence with, after
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 XX isolated nucleic acids of the invention are useful as probes and primers
 XX for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 XX e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 XX and for production of recombinant polypeptides. Any of the nucleic acids,
 XX polypeptides, vectors containing the nucleic acids, cells containing the
 XX vector or antibodies directed against the polypeptides are useful for
 XX preparation of pharmaceuticals for prevention and/or treatment of viral
 XX diseases that are characterised by development of tumours or cell
 XX degeneration, specifically cancer but also Alzheimer's disease and
 XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 XX patient samples is useful for diagnosis and/or prognosis of these
 XX diseases. The polypeptides can also be used to generate antibodies, and
 XX both the polypeptide and antibodies are useful as components of protein
 XX chips. The nucleic acid sequences of the invention can be used in gene
 XX therapy. This polynucleotide sequence represents a tumour suppression
 XX related human fukutin oligonucleotide of the invention.

Sequence 17 BP; 5 A; 2 C; 2 G; 8 T; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1292 ATCTCAATTTTAAT 1307
 |||||
 2 ATCTCAATTTTAAT 17

DB 2 ATCTCAATTTTAAT 17

RESULT 577
 ABT39979/c
 ID ABT39979 standard; DNA; 17 BP.
 XX ABT39979;
 XX ABT39979;
 XX 13-JUN-2003 (first entry)
 XX Tumour suppression related human fukutin oligo SEQ ID No 5616.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 XX schizophrenia; protein chip; gene therapy; tumour suppression;
 XX human fukutin; ds.
 XX Homo sapiens.
 XX WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB04208.

{ Mcswiggen J;
 { WPI; 2003-140484/13.
 { Novel short interfering RNA and enzymatic nucleic acid useful for
 { treating cancer, modulates the expression of a nucleic acid encoding
 { HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 { Claim 58; Page 91; 185pp; English.
 { The invention relates to a novel short interfering RNA (siRNA) nucleic
 { acid molecule or an enzymatic nucleic acid molecule, that modulates
 { expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 { human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 { acid molecule of the invention has cytostatic, anti-HIV, and
 { anti-rheumatic activity. The nucleic acid molecules are useful for
 { reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 { acids are also useful for treating breast, ovarian, colorectal, lung,
 { prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 { The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
 { ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
 { sequences for the human ribozymes of the invention.
 { Sequence 17 BP; 8 A; 1 C; 1 G; 7 U; 0 other;
 { Query Match 1.0%; Score 12.8; DB 1; Length 17;
 { Best Local Similarity 50.0%; Pred. No. 4.3e+02;
 { Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 { 1176 TTAGATAAATTTCAAT 1191
 { :|||:||||:|:
 { 1 UUGAUAUAUUCUAD 16
 { SUIT 580
 { Z60265/c
 { ABZ60265 standard; RNA; 17 BP.
 { ABZ60265;
 { 21-MAR-2003 (first entry)
 { Human K-Ras DNzyme substrate #377.
 { Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 { enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 { anti-rheumatic; cancer; AIDS; ss.
 { Homo sapiens.
 { WO200297114-A2.
 { 05-DEC-2002.
 { 29-MAY-2002; 2002WO-US16840.
 { 29-MAY-2001; 2001US-294140P.
 { 06-JUN-2001; 2001US-296249P.
 { 10-SEP-2001; 2001US-318471P.
 { (RIBO-) RIBOZYME PHARM INC.
 { Mcswiggen J;
 { WPI; 2003-140484/13.
 { Novel short interfering RNA and enzymatic nucleic acid useful for
 { treating cancer, modulates the expression of a nucleic acid encoding
 { HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 { Claim 58; Page 92; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and
 CC anti-rheumatic activity. The nucleic acid molecules are useful for
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 CC acids are also useful for treating breast, ovarian, colorectal, lung,
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
 CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
 CC sequences for the human ribozymes of the invention.
 CC Sequence 17 BP; 7 A; 0 C; 3 G; 7 U; 0 other;
 CC Query Match 1.0%; Score 12.8; DB 1; Length 17;
 CC Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 CC Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 627 CAATAAATTTTGAAT 642
 Db 16 CAATAAATCTTTAAT 1
 RESULT 581
 ABZ60471/c
 ID ABZ60471 standard; RNA; 17 BP.
 XX AC ABZ60471;
 XX 21-MAR-2003 (first entry)
 XX Human K-Ras DNzyme substrate #583.
 XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 XX anti-rheumatic; cancer; AIDS; ss.
 XX Homo sapiens.
 XX WO200297114-A2.
 XX 05-DEC-2002.
 XX 29-MAY-2002; 2002WO-US16840.
 XX 29-MAY-2001; 2001US-294140P.
 XX 06-JUN-2001; 2001US-296249P.
 XX 10-SEP-2001; 2001US-318471P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Mcswiggen J;
 XX WPI; 2003-140484/13.
 XX Novel short interfering RNA and enzymatic nucleic acid useful for
 XX treating cancer, modulates the expression of a nucleic acid encoding
 XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 XX Claim 58; Page 96; 185pp; English.
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 XX acid molecule or an enzymatic nucleic acid molecule, that modulates
 XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 XX acid molecule of the invention has cytostatic, anti-HIV, and
 XX anti-rheumatic activity. The nucleic acid molecules are useful for
 XX reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 XX acids are also useful for treating breast, ovarian, colorectal, lung,
 XX prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 XX The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
 XX ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target

C sequences for the human ribozymes of the invention.

X Sequence 17 BP; 5 A; 1 C; 2 G; 9 U; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 4.3e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1392 TTAGACTATTAAAC 1407

b 16 TTACAGTATTAAAC 1

RESULT 582

BZ60554/C

D ABZ60554 standard; RNA; 17 BP.

X ABZ60554;

C ABZ60554;

X ABZ60554;

I 21-MAR-2003 (first entry)

X Human K-Ras DNzyme substrate #666.

E Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

M enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;

N anti-rheumatic; cancer; AIDS; ss.

I Homo sapiens.

S WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

X WO200297114-A2.

PF 29-MAY-2002; 2002WO-US16840.

PX

PR 29-MAY-2001; 2001US-294140P.
06-JUN-2001; 2001US-296249P.

PR 10-SEP-2001; 2001US-318471P.

PX

PA (RIBO-) RIBOZYME PHARM INC.

PX

PI Mcswiggen J;

PX WPI; 2003-140484/13.

DR

PT Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras,

PT

PX Claim 58; Page 108; 185pp; English.

PS

PX The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ65524, ABZ66530 - ABZ66585 represent substrate/target sequences for the human ribozymes of the invention.

CC

XX Sequence 17 BP; 4 A; 2 C; 3 G; 8 U; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 43.8%; Pred. No. 4.3e+02;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps

QY 1051 TGTATTATTTAAAGCA 1066
DB :|::||:: ||
 2 UGUUUUAUUGCA 17

RESULT 586
ABZ61149/c
ID ABZ61149 standard; RNA; 17 BP.
AC
AC ABZ61149;
XX
DT 21-MAR-2003 (first entry)
XX Human K-Ras DNAzyme substrate #1261.
DE
DE Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
CS Homo sapiens.
XX WO200297114-A2.
PX PD
PD 05-DEC-2002..
XX
PP 29-MAY-2002; 2002WO-US16840.
XX
XX 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
PI Mcswiggen J;
PX
DX WPI; 2003-140484/13.

X Novel short interfering RNA and enzymatic nucleic acid useful for
 T treating cancer, modulates the expression of a nucleic acid encoding
 T HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 X Claim 58; Page 109; 185pp; English.
 X The invention relates to a novel short interfering RNA (siRNA) nucleic
 C acid molecule or an enzymatic nucleic acid molecule, that modulates
 C expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 C human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 C acid molecule of the invention has cytostatic, anti-HIV, and
 C anti-rheumatic activity. The nucleic acid molecules are useful for
 C reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 C acids are also useful for treating breast, ovarian, colorectal, lung,
 C prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 C The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
 C ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
 C sequences for the human ribozymes of the invention.
 X Sequence 17 BP; 6 A; 4 C; 2 G; 5 U; 0 other;
 Q Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 4.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Y 796 TTTTGCATTAAGTCA 811
 b ||||| ||||| ||
 17 TTTTGTCTAATAGGCA 2
 RESULT 587
 BZ61155
 D ABZ61155 standard; RNA; 17 BP.
 X X ABZ61155;
 C ABZ61155;
 T 21-MAR-2003 (first entry)
 T Human K-Ras DNzyme substrate #1267.
 X Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 W enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 W anti-rheumatic; cancer; AIDS; ss.
 X Homo sapiens.
 X WO200297114-A2.
 X 05-DEC-2002.
 X 29-MAY-2002; 2002WO-US16840.
 X 29-MAY-2001; 2001US-294140P.
 R 06-JUN-2001; 2001US-296249P.
 R 10-SEP-2001; 2001US-318471P.
 X (RIBO-) RIBOZYME PHARM INC.
 X Mcswiggen J;
 X WPI; 2003-140484/13.
 X Novel short interfering RNA and enzymatic nucleic acid useful for
 T treating cancer, modulates the expression of a nucleic acid encoding
 T HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 X Claim 58; Page 109; 185pp; English.
 X The invention relates to a novel short interfering RNA (siRNA) nucleic
 C acid molecule or an enzymatic nucleic acid molecule, that modulates
 C expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 C human immunodeficiency virus (HIV) or a component of HIV. The nucleic

CC acid molecule of the invention has cytostatic, anti-HIV, and
 CC anti-rheumatic activity. The nucleic acid molecules are useful for
 CC reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 CC acids are also useful for treating breast, ovarian, colorectal, lung,
 CC prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 CC The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
 CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
 CC sequences for the human ribozymes of the invention.
 X Sequence 17 BP; 7 A; 1 C; 0 G; 9 U; 0 other;
 Q Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 43.8%; Pred. No. 4.3e+02;
 Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
 Y 1002 ATAACATATAATTTT 1017
 b ||||| ||||| |||||
 1 AUAACAUAUUUAUUU 16
 RESULT 588
 ABZ61203
 ID ABZ61203 standard; RNA; 17 BP.
 X X ABZ61203;
 AC ABZ61203;
 DT 21-MAR-2003 (first entry)
 DE Human K-Ras DNzyme substrate #1315.
 X Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 X enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 X anti-rheumatic; cancer; AIDS; ss.
 X Homo sapiens.
 X WO200297114-A2.
 X 05-DEC-2002.
 X 29-MAY-2002; 2002WO-US16840.
 X 29-MAY-2001; 2001US-294140P.
 PR 06-JUN-2001; 2001US-296249P.
 PR 10-SEP-2001; 2001US-318471P.
 X (RIBO-) RIBOZYME PHARM INC.
 X Mcswiggen J;
 X WPI; 2003-140484/13.
 X Novel short interfering RNA and enzymatic nucleic acid useful for
 T treating cancer, modulates the expression of a nucleic acid encoding
 T HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 X Claim 58; Page 110; 185pp; English.
 X The invention relates to a novel short interfering RNA (siRNA) nucleic
 C acid molecule or an enzymatic nucleic acid molecule, that modulates
 C expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 C human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 C acid molecule of the invention has cytostatic, anti-HIV, and
 C anti-rheumatic activity. The nucleic acid molecules are useful for
 C reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 C acids are also useful for treating breast, ovarian, colorectal, lung,
 C prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 C The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531,
 CC ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
 CC sequences for the human ribozymes of the invention.
 X Sequence 17 BP; 5 A; 1 C; 0 G; 11 U; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 25.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

598 TATTATTATTGGAT 613
 1 UAGUAGUAGUUCUAD 16

RESULT 509
 ABZ61621 standard; RNA; 17 BP.
 ABZ61621;
 21-MAR-2003 (first entry)
 Human H-Ras DNAzyme target #412.
 Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
 anti-rheumatic; cancer; AIDS; ss.
 Homo sapiens.
 WO200297114-A2.
 05-DEC-2002.
 29-MAY-2002; 2002WO-US16840.
 29-MAY-2001; 2001US-294140P.
 06-JUN-2001; 2001US-296249P.
 10-SEP-2001; 2001US-318471P.
 (RIBO-) RIBOZYME PHARM INC.
 Mcswiggen J;
 WPI; 2003-140484/13.
 Novel short interfering RNA and enzymatic nucleic acid useful for
 treating cancer, modulates the expression of a nucleic acid encoding
 HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
 Claim 58; Page 118; 185pp; English.
 The invention relates to a novel short interfering RNA (siRNA) nucleic
 acid molecule or an enzymatic nucleic acid molecule, that modulates
 expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 acid molecule of the invention has cytosstatic, anti-HIV, and
 anti-rheumatic activity. The nucleic acid molecules are useful for
 reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic
 acids are also useful for treating breast, ovarian, colorectal, lung,
 prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS.
 The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531.
 ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target
 sequences for the human ribozymes of the invention.

Sequence 17 BP; 3 A; 3 C; 5 G; 6 U; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 62.5%; Pred. No. 4.3e+02;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

818 GCTGGAATCTGGAT 833
 2 GUUGACACUCCUGAU 17

RESULT 590
 AT43555

ID AAT43555 standard; DNA; 18 BP.
 XX AC AAT43555;
 XX
 DT 18-JUL-1997 (first entry)
 XX
 DE HUMTH01 microsatellite Bp allele PCR primer 5.
 XX
 KW Human; Homo sapiens; tyrosine hydroxylase; HUMTH01; schizophrenia;
 KW diagnosis; subtyping; predisposition; polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 XX WO9634980-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 29-APR-1996; 96WO-FR00650.
 XX
 PR 03-MAY-1995; 95FR-0005264.
 XX
 XX (RHON) RHONE POULENC RORER SA.
 XX
 XX Laurent C, Mallet J, Meloni R;
 XX
 XX WPI; 1996-506180/50.
 XX
 PT Diagnosing schizophrenia by detecting tyrosine hydroxylase Bp allele
 PT - using new PCR primers, also for genetic characterisation and
 PT detection of pre-disposition to schizophrenia
 XX
 PS Example 4; Page 10; 30pp; French.
 XX
 CC Schizophrenia can be diagnosed by detecting in vitro presence of the
 CC Bp allele of the microsatellite HUMTH01 in the tyrosine hydroxylase
 CC gene. In particular, pairs of primers are used in a polymerase chain
 CC reaction for amplifying a fragment of less than 300 bp comprising
 CC HUMTH01 and a flanking sequence. Specific primer pairs suitable for
 CC amplifying the microsatellite contain primers 1 and 2 (AAT43552 and
 CC AAT43553), primers 1 and 4 (AAT43552 and AAT43554) or primers 5 and 6
 CC (AAT43555 and AAT43556). The method is used for diagnosis, genetic
 CC characterisation and subtyping of schizophrenia and to detect
 CC predisposition to this disease. It may also allow better selection
 CC of treatments for schizophrenia.
 XX
 SQ Sequence 18 BP; 1 A; 8 C; 1 G; 8 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 4.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 905 GTTCTCTCTTATTC 920
 Db 1 GTTCTCTCTTATTC 16

RESULT 591
 AAV60776
 ID AAV60776 standard; DNA; 18 BP.
 XX
 AC AAV60776;
 XX
 DT 25-MAR-2003 (updated)
 DT 08-DEC-1998 (first entry)
 XX
 XX HIV-1 strain YBF30 pol gene primer YRT2-2.
 XX
 KW HIV-1 strain YBF30; antibody; oligonucleotide; diagnosis; immunisation;
 KW infection; typing; poi; PCR primer; amplification; ss.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus type 1.

N FR2756843-A1.
 X 12-JUN-1998.
 X 09-DEC-1996; 96FR-0015087.
 X 09-DEC-1996; 96FR-0015087.
 R (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
 A (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 A (INSP) INST PASTEUR.
 X Mauciere P, Lousseret AI, Simon F, Saragosti S, Barre SF;
 X WPI; 1998-336114/30.
 R Non-M, non-O HIV-1 strain YBP30 - useful for diagnosis and
 X immunisation
 T Claim 3; Fig 1; 85pp; French.
 X This sequence represents a primer targeted to the pol gene of the non-M
 X (major), non-O (Outlier) HIV-1 strain YBP30 (NCIM I-1753), isolated from
 C the Cameroon. The HIV strain (see AAV60751 for complete genome),
 C peptides, antibodies and oligonucleotides derived from it (see
 C AAV60752-V60798 and AAW68473-W68482) are used for diagnosis of or
 C immunisation against non-M, non-O HIV-1 infections. The
 C oligonucleotides, peptides and antibodies can also be used for typing HIV
 C strains.
 C (Updated on 25-MAR-2003 to correct PI field.)
 X Sequence 18 BP; 6 A; 4 C; 4 G; 4 T; 0 other;
 Q Query Match 1.0%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 4.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Y 410 TATCCAGGATCACTG 425
 b ||||| ||||| |||||
 3 TATCCAGGATCACTG 18
 RESULT 592
 AAV49122
 D AAV49122 standard; DNA; 18 BP.
 X
 X AAV49122;
 X 15-OCT-1998 (first entry)
 X rb gene antisense oligonucleotide rb-N-70.
 X rb gene; antisense oligonucleotide; modulate; gene expression; ss.
 X Synthetic.
 X Homo sapiens.
 X EP856579-A1.
 X 05-AUG-1998.
 X 31-JAN-1997; 97EP-0101531.
 X 31-JAN-1997; 97EP-0101531.
 X (BIOG-) BIOGOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 X Brysch W, Schlingensiepen K;
 X WPI; 1998-400910/35.
 X Preparation of antisense oligonucleotide(s) which lack long runs of
 PT consecutive guanosine or inosine - and have specific ratio of

PT residues able to form two or three hydrogen bonds, have greater
 PT activity and reduced toxicity, used therapeutically or to modulate
 PT growth of cells in culture
 XX Example 7; Fig 9b; 286pp; English.
 XX
 CC AAV49008-236 represent antisense oligonucleotides directed against
 CC the rb gene. Of these, only oligonucleotides AAV49008-52 resulted in
 CC effective downregulation of negative growth control by rb, while
 CC oligonucleotides AAV49052-236 had little effect. The oligonucleotides
 CC exemplify the invention. The specification describes oligonucleotides
 CC that contain 8-30 nucleotides, which contain at most 8 nucleotides
 CC that can each form three hydrogen bonds to cytosine; do not contain
 CC four consecutive nucleotides able to form three H-bonds each to four
 CC consecutive cytosines; do not contain two sequences of three consecutive
 CC nucleotides each able to form three H-bonds to three consecutive
 CC cytosines, and the ratio between residues able to form two H-bonds
 CC each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
 CC oligonucleotides are used to modulate expression of genes, particularly
 CC the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or beta 2 to control
 CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
 CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
 CC oligonucleotides can also be used to analyse function of proteins (by
 CC altering their expression or activity) and therapeutically, e.g. in
 CC cases of cancer or (targeting TGF) for stimulating the immune system.
 X Sequence 18 BP; 6 A; 1 C; 1 G; 10 T; 0 other;
 Q Query Match 1.0%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 4.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1173 TTATTAGATAAATTC 1188
 ||||| ||||| |||||
 1 TTATTAGATAAATTC 16
 Db
 RESULT 593
 AAV36410
 ID AAV36410 standard; CDNA; 18 BP.
 X
 X AAV36410;
 X 14-SEP-1998 (first entry)
 X Antisense oligonucleotide 15 directed at DHFR.
 X Oligonucleotide; Antisense; synthetic; pfmdr;
 X Plasmodium falciparum multi-drug resistance gene (II); resensitise;
 X drug-resistant; malaria; mefloquine; quinine; DHFR;
 X thymidylate synthase; ss.
 X Synthetic.
 X Plasmodium falciparum.
 X WO98213223-A2.
 X 22-MAY-1998.
 X 12-NOV-1997; 97WO-US20590.
 X 12-NOV-1996; 96US-0745485.
 X (HYBR-) HYBRIDON INC.
 X (WORC-) WORCESTER FOUND BIOMEDICAL RES.
 X Baker RH, Rapaport E, Zamecnik PC;
 X WPI; 1998-297928/26.
 X New synthetic oligonucleotide(s) anti-sense to multi-drug
 PT resistance gene of Plasmodium - useful for, e.g. restoring
 PT sensitivity to anti-malarial drugs such as mefloquine and quinine

Examples; Page 48; 75pp; English.

Antisense oligonucleotide AAV36410 was used to target the DHFR gene from Plasmodium falciparum. This oligonucleotide corresponds to an internal portion of the 27mer AAV36406 (directed at a conserved sequence in the thymidylate synthase portion of the DHFR gene from bp 1153-1179), which had previously been shown to be highly inhibitory, in vitro, to Plasmodium falciparum. AAV36396-V36404 oligonucleotides were targeted at the pfmdr1 gene bind to the targeted DNA molecule and thereby prevent the normal action of the target molecule. The synthetic oligonucleotides are complementary to pfmdr1 (Plasmodium falciparum multi-drug resistance gene (II)), and are used to resensitize an infectious organism to a drug that had prior become drug-resistant. Therefore the application of these oligonucleotides to the pfmdr1 gene allows the reuse of many anti-malarial drugs.

Sequence 18 BP; 7 A; 2 C; 2 G; 7 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1259 AATAAATTTTCTTACTA 1274
|||||||
2 AATAAATTTTCTTCTGTA 17

SULT 594
V36411/C

AAV36411 standard; cDNA; 18 BP.

AAV36411;

14-SEP-1998 (first entry)

Sense oligonucleotide 16 directed at DHFR.

Oligonucleotide; Antisense; synthetic; pfmdr;
Plasmodium falciparum multi-drug resistance gene (II); resensitise;
drug-resistant; malaria; mefloquine; quinine; DHFR;
thymidylate synthase; ss.

Synthetic.

Plasmodium falciparum.

WO9821323-A2.

22-MAY-1998.

12-NOV-1997; 97WO-US20590.

12-NOV-1996; 96US-0745485.

(HYBR-) HYBRIDON INC.

(WORC-) WORCESTER FOUND BIOMEDICAL RES.

Baker RH, Rapaport E, Zamecnik PC;

WPI; 1998-297928/26.

New synthetic oligo:nucleotide(s) anti-sense to multi-drug resistance gene of Plasmodium - useful for, e.g. restoring sensitivity to anti-malarial drugs such as mefloquine and quinine

Examples; Page 48; 75pp; English.

Sense oligonucleotide AAV36411 is complementary to the antisense oligonucleotide AAV36410. It was used to target the DHFR gene from Plasmodium falciparum and served as a sense strand control for sequence specificity. The complementary antisense oligonucleotide AAV36410 corresponds to an internal portion of the 27mer AAV36406 (directed at a conserved sequence in the thymidylate synthase portion of the DHFR gene

from bp 1153-1179), which had previously been shown to be highly inhibitory, in vitro, to Plasmodium falciparum. AAV36396-V36404 oligonucleotides were targeted at the pfmdr1 gene bind to the targeted DNA molecule and thereby prevent the normal action of the target molecule. The synthetic oligonucleotides are complementary to pfmdr1 (Plasmodium falciparum multi-drug resistance gene (II)), and are used to resensitize an infectious organism to a drug that had prior become drug-resistant. Therefore the application of these oligonucleotides to the pfmdr1 gene allows the reuse of many anti-malarial drugs.

Sequence 18 BP; 7 A; 2 C; 2 G; 7 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 4.5e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1259 AATAAATTTTCTTACTA 1274
|||||||
DB 17 AATAAATTTCTTCTGTA 2

RESULT 595
AAV34526

ID AAV34526 standard; DNA; 18 BP.

XX AAV34526;

XX 20-AUG-1998 (first entry)

Chemokine receptor CXCR4 amplifying RT-PCR primer 2.

Chemokine receptor; gpl20; fusion protein; HIV; screening; AIDS;

CD4 binding site; RT-PCR primer; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9815569-A1.

XX 16-APR-1998.

XX 08-OCT-1997; 97WO-US18397.

XX 09-OCT-1996; 96US-0027931.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX (DAND) DANA FARBEN CANCER INST INC.

XX (LEUK-) LEUKOSITE INC.

XX Gerard C, Gerard N, Newman W, Sodroski J, Wu L;

XX WPI; 1998-240778/21.

XX Derivatives of gpl20 containing modified chemokine receptor binding site - and complexes with soluble CD40, for inhibiting infectivity of human immune deficiency virus and to screen for inhibitors

XX Examples; Page 53; 92pp; English.

XX This primer is used for the RT-PCR amplification of a chemokine receptor CXCR4. The invention provides gpl20 derivative having a conformational, discontinuous chemokine receptor binding site defined by amino acids residues present in the gpl20 constant regions C2, C3 and C4, and the variable region V3, and its conformation is similar to that of the receptor binding site of wild-type gpl20 complexed to CD4. Exposure of the chemokine receptor binding site is increased by having at least part of a variable or constant region of wild-type gpl20 removed. A stabilised complex of gpl20 CD4 binding site with a soluble CD4 molecule is used to inhibit infectivity of human immune deficiency virus (HIV). Labelled gpl20 derivatives are also used to screen for inhibitors of HIV infectivity. The gpl20 derivatives are used for diagnosing susceptibility to HIV infection from increased levels of the chemokine receptors (at the protein or nucleic acid levels). Transgenic animals expressing CD4 and

C chemokine receptor are used as models for studying development of AIDS or
C effect/safety of therapeutic agents.

X Q Sequence 18 BP; 4 A; 4 C; 7 G; 3 T; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 485 GTGTAGGTTGCCAG 500
|||||
b 1 GTGTAGGCGCCAG 16

RESULT 596
AAZ41004/C
D AAZ41004 standard; DNA; 18 BP.
X C AAZ41004;
X C 26-JAN-2000 (first entry)
T Human RhoC phosphorothioate antisense oligonucleotide SEQ ID NO:156.

E Identification; genetic target; gene modulation; human; probe;
W antisense oligonucleotide; phosphorothioate; PCR primer;
W nucleotide sequence-based technology; antisense drug discovery;
W target validation; ss.

X Synthetic.
S Homo sapiens.
S WO9953101-A1.
X 21-OCT-1999.
X 13-APR-1999; 99WO-US08268.

X 13-APR-1998; 98US-0081483.
X 28-APR-1998; 98US-0067638.
X (ISIS-) ISIS PHARM INC.

X Cowsett LM, Baker BF, McNeil J, Freier SM, Sasamor HM, Brooks DG;
X Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
X WPI; 1999-620446/53.
X Identifying compounds which modulate expression of nucleic acids, used
X to provide compounds having defined physical, chemical or bioactive
X properties, e.g. antisense activity -

X Example 18; Page 97; 264pp; English.
X A method has been developed of defining a set of compounds that modulate
X the expression of a target nucleic acid (tNA) sequence via binding of
X the compounds with the tNA sequence. The method comprises generating a
X library of virtual compounds in silico according to defined criteria,
X and evaluating in silico the binding of the virtual compounds with the
X tNA according to defined criteria. Also described are: (1) a method of
X defining a set of oligonucleotides (ONS) that modulate the expression of
X a tNA sequence via binding of the ONS with the tNA sequence comprising
X generating a library of virtual compounds in silico according to defined
X criteria, and evaluating in silico the binding of the virtual ONS with
X the tNA according to defined criteria; and (2) a method of defining a
X set of compounds that modulate the expression of a tNA sequence via
X binding of the compounds with the tNA. The methods can be used for the
X generation and identification of synthetic compounds having defined
X physical, chemical or bioactive properties. Information gathered from
X assays of such compounds is used to identify nucleic acid sequences that
X are tractable to a variety of nucleotide sequence-based technologies,
X e.g. antisense drug discovery and target validation. AAZ40852 to
X AAZ41220, and AAZ52701 to AAZ52706, represent sequences used in the

CC exemplification of the present invention.

XX Sequence 18 BP; 7 A; 5 C; 4 G; 2 T; 0 other;

QY Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 827 CCTGGATTTTCTCTG 842
|||||
Db 18 CCTGGAGTTTCTCTG 3

RESULT 597
AAXS6787/C
ID AAXS6787 standard; DNA; 18 BP.

XX AAXS6787;
XX 14-JUL-1999 (first entry)
DT WO9922023 probe 23.

XX Microorganism; hybridisation; probe; identification; detection;
XX bacteria; milk; water; automated; ss.
XX Synthetic.
XX WO9922023-A2.

XX 06-MAY-1999.
XX 29-OCT-1998; 98WO-EP06863.
XX 29-OCT-1997; 97DE-1047731.
XX (MIRA-) MIRA DIAGNOSTICA GMBH.

XX Epping B, Leiser M;
XX WPI; 1999-303024/25.
XX Identifying specific microorganisms present in a mixture
XX Claim 1; Page 8; 19pp; German.

XX This invention describes the detection of specific microorganisms from
XX various taxa, in a sample containing several different microorganisms by
XX nucleic acid hybridization, using as probes, 62 specific
XX oligonucleotides (represented in AAXS6785-XS8826) with at least one
XX oligonucleotide being able to hybridize to each microorganism. The method
XX is useful for detecting and identifying bacteria in milk and water. The
XX method, which may be fully automated, allows simultaneous detection and
XX unequivocal identification of bacteria from different taxa.

XX Sequence 18 BP; 5 A; 5 C; 3 G; 5 T; 0 other;

QY Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 726 TTTCAGGAATTCGATG 741
|||||
Db 17 TTTCAGGAATTCGATG 2

RESULT 598
AAX37761/C
ID AAX37761 standard; DNA; 18 BP.

XX AAX37761;
XX 09-JUL-1999 (first entry)

Staphylococcus sp. detecting oligonucleotide fsg2s.
 FemA; primer; identification; detection; therapy; infection; femB;
 amplification; genotyping; gram-positive bacteria; vaccine; ss.
 Synthetic.
 Staphylococcus sp.
 WO9916780-A2.
 08-APR-1999.
 28-SEP-1998; 98WO-BE00141.
 26-SEP-1997; 97EP-0870146.
 (BENA-) BELGIAN MIN NAT DEFENCE.
 (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 Gala J, Vannuffel P;
 WPI; 1999-287521/24.
 New Staphylococcus-specific oligonucleotides
 Claim 5; Page 8; 48pp; English.
 This invention describes novel Staphylococcus-specific oligonucleotides
 based on the consensus femA nucleotide sequence which are used to
 develop products for the identification, detection and therapy of
 infections. The oligonucleotides can be used for the genetic
 amplification, the identification and/or quantification of various femA
 sequences which are specific to known or unknown Staphylococci species.
 Since the femA sequence is similar to the femB sequence, the
 oligonucleotides can also be used for the molecular genotyping of femB
 genes of different Staphylococci species or other gram-positive bacteria.
 The femA nucleic acids can also be used in therapeutic applications.
 They can also be used to identify inhibitors, e.g. antibodies or
 antisense oligonucleotides, for blocking expression of the femA
 nucleotide sequences. They can also be used for producing vaccines
 against Staphylococci infections.
 Sequence 18 BP; 12 A; 1 C; 3 G; 2 T; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. NO. 4.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1562 ATTTTCTTACTGTTT 1577
 |||||
 16 ATTTTCTTACTGTTT 1
 |||||
 RESULT 599
 AV82030/C
 AAV82030 standard; DNA; 18 BP.
 AAV82030;
 21-JUN-1999 (first entry)
 Moraxella lactoferrin binding protein 1 (Lbp1) PCR primer.
 Lactoferrin receptor; lactoferrin binding protein; Lbp1;
 lbpA gene; infection; otitis media; sinusitis; conjunctivitis;
 pneumonia; bronchitis; tracheitis; emphysema; diagnosis; therapy;
 vaccine; Branhamella catarrhalis; PCR; primer; ss.
 Synthetic.
 Moraxella catarrhalis.
 WO9855606-A2.

XX 10-DEC-1998.
 PD 02-JUN-1998; 98WO-CA00544.
 XX 08-MAY-1998; 98US-0074658.
 PR 03-JUN-1997; 97US-0867941.
 XX (CONN-) CONNAUGHT LAB LTD.
 XX Du R, Klein MH, Loosmore SM, Wang Q, Yang Y;
 XX WPI; 1999-070266/06.
 XX Lactoferrin receptor genes from Moraxella, especially M. catarrhalis
 PT - useful to diagnose Moraxella infection e.g. to detect otitis media
 PT due to M. catarrhalis infection and to immunise against such
 PT infections
 XX
 PS Example 1; Page 37; 202pp; English.
 XX This PCR primer is based on a C-terminal peptide (see AAW89423) of
 CC Moraxella catarrhalis lactoferrin binding protein 1 (Lbp1). PCR
 CC primers (see AAV82030-31) based on this C-terminal peptide and other
 CC primers (see AAV82022-29) based on an isolated N-terminal peptide,
 CC are used in the amplification of M. catarrhalis lbpA genes that
 CC code for Lbp1. The invention provides immunogenic compositions,
 CC including vaccines, based upon expressed recombinant lbp1 and/or
 CC lbp2 and/or ORF3 proteins (see AAW89413-21) for use in the prevention
 CC of diseases (e.g. otitis media) caused by Moraxella. The genes and
 CC DNA sequences of the Moraxella lactoferrin receptor (lfr) locus
 CC (see AAV82019-21) are useful for diagnosis, immunisation, and the
 CC generation of diagnostic and immunological reagents.
 XX
 SQ Sequence 18 BP; 7 A; 1 C; 3 G; 7 T; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. NO. 4.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1233 TTAAATTTTCAATTTCA 1248
 |||||
 DB 18 TTAAATTTTCAATTTCA 3
 |||||
 RESULT 600
 AAV82031
 ID AAV82031 standard; DNA; 18 BP.
 XX
 AC AAV82031;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Moraxella lactoferrin binding protein 1 (Lbp1) PCR primer.
 XX Lactoferrin receptor; lactoferrin binding protein; Lbp1;
 KW lbpA gene; infection; otitis media; sinusitis; conjunctivitis;
 KW pneumonia; bronchitis; tracheitis; emphysema; diagnosis; therapy;
 KW vaccine; Branhamella catarrhalis; PCR; primer; ss.
 XX
 OS Synthetic.
 OS Moraxella catarrhalis.
 XX
 PN WO9855606-A2.
 XX
 PD 10-DEC-1998.
 XX 02-JUN-1998; 98WO-CA00544.
 XX 08-MAY-1998; 98US-0074658.
 PR 03-JUN-1997; 97US-0867941.
 XX (CONN-) CONNAUGHT LAB LTD.

CC Du R, Klein MH, Loosmore SM, Wang Q, Yang Y;
 CC WPI; 1999-070266/06.
 CC Lactoferrin receptor genes from Moraxella, especially M. catarrhalis
 CC - useful to diagnose Moraxella infection e.g. to detect otitis media
 CC due to M. catarrhalis infection and to immunise against such
 CC infections
 CC Example 1; Page 37; 202pp; English.
 CC This PCR primer is based on a C-terminal peptide (see AAV89423) of
 CC Moraxella catarrhalis lactoferrin binding protein 1 (Lbp1). PCR
 CC primers (see AAV82030-31) based on this C-terminal peptide and other
 CC primers (see AAV82022-29) based on an isolated N-terminal peptide,
 CC are used in the amplification of M. catarrhalis lbpA genes that
 CC code for Lbp1. The invention provides immunogenic compositions,
 CC including vaccines, based upon expressed recombinant Lbp1 and/or
 CC Lbp2 and/or ORF3 proteins (see AAV89413-21) for use in the prevention
 CC of diseases (e.g. otitis media) caused by Moraxella. The genes and
 CC DNA sequences of the Moraxella lactoferrin receptor (lfr) locus
 CC (see AAV82019-21) are useful for diagnosis, immunisation, and the
 CC generation of diagnostic and immunological reagents.
 CC Sequence 18 BP; 7 A; 3 C; 1 G; 7 T; 0 other;
 CC
 CC Query Match 1.0%; Score 12.8; DB 1; Length 18;
 CC Best Local Similarity 87.5%; Pred. NO. 4.5e+02;
 CC Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC 1233 TTAATTTTCATTCA 1248
 CC 1 TTAATTTTCATTCA 16
 CC
 CC RESULT 601
 CC AAX27574
 CC ID AAX27574 standard; DNA; 18 BP.
 CC AAX27574;
 CC 27-MAY-1999 (first entry)
 CC RT-PCR primer RT-NTENA7.
 CC Influenza antigen; fusion product; extracellular; membrane protein;
 CC M2 protein; vaccine; human; animal; pig; horse; RT-PCR; primer; ss.
 CC Synthetic.
 CC WO9907839-A2.
 CC 18-FEB-1999.
 CC 05-AUG-1998; 98WO-EP05106.
 CC 05-AUG-1997; 97EP-0202434.
 CC (VLAA-) VLAAHS INTERUNIVERSITAIR INST BIOTECHNOG.
 CC Fiers W, Min Jou W, Neirynck S;
 CC WPI; 1999-167418/14.
 CC New influenza antigens for use in vaccines - comprising a fusion
 CC product of the extracellular part of a conserved influenza membrane
 CC protein and a presenting carrier
 CC Disclosure; Fig 29; 100pp; English.
 CC The invention relates to new influenza antigens that comprise a fusion
 CC product of at least the extracellular part of a conserved influenza

CC membrane protein (or a functional fragment) and a presenting carrier.
 CC The membrane protein consists of the extracellular part of the influenza
 CC M2 protein. The influenza antigens can be used in the preparation of a
 CC vaccine against influenza for humans and animals, e.g. pigs and horses.
 CC The vaccines can be direct vaccines, e.g. vaccines containing the fusion
 CC products or indirect, DNA vaccines.
 CC Sequence 18 BP; 7 A; 0 C; 6 G; 5 T; 0 other;
 CC
 CC Query Match 1.0%; Score 12.8; DB 1; Length 18;
 CC Best Local Similarity 87.5%; Pred. NO. 4.5e+02;
 CC Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC 1155 TAGATATTGAATGATG 1170
 CC 3 TAGATATTGAATGATG 18
 CC
 CC RESULT 602
 CC AAZ70894/C
 CC ID AAZ70894 standard; DNA; 18 BP.
 CC AAZ70894;
 CC 10-SEP-2001 (first entry)
 CC Human biallelic marker upstream amplification primer SEQ ID NO:5250.
 CC Human genome; biallelic marker; high density disequilibrium map;
 CC genomic map; haplotype; phenotype; polymorphic base; genotyping;
 CC haplotyping; hybridisation; identification; characterisation;
 CC amplification; single nucleotide polymorphism; SNP; PCR primer;
 CC diagnosis; ss.
 CC Homo sapiens.
 CC WO9954500-A2.
 CC 28-OCT-1999.
 CC 21-APR-1999; 99WO-IB00822.
 CC 21-APR-1998; 98US-0082614.
 CC 23-NOV-1998; 98US-0109732.
 CC (GBST) GENSET.
 CC Cohen D, Blumenfeld M, Chumakov I;
 CC WPI; 2000-013267/01.
 CC Novel biallelic markers used to construct a high density disequilibrium
 CC map of the human genome -
 CC Claim 8; Page 1350; 2745pp; English.
 CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the
 CC invention have a variety of uses: they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other
 CC treatment.
 CC N.B. The SEQ ID NOS 2913, 2974, 3035, 3096, 3157, 3237, 3297
 CC and 3367, are not actually given a sequence in the Sequence listing
 CC from the present invention.


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} Sequence 18 BP; 6 A; 6 C; 3 G; 3 T; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

820 TGGAAATCTCGATT 835
|||||
17 TGGAAAGCTCGTTT 2

RESULT 603
AAZ71730
AAZ71730 standard; DNA; 18 BP.
AAZ71730;
10-SEP-2001 (first entry)
Human biallelic marker upstream amplification primer SEQ ID NO:6086.
Human genome; biallelic marker; high density disequilibrium map;
genomic map; haplotype; phenotype; polymorphic base; genotyping;
haplotyping; hybridisation; identification; characterisation;
amplification; single nucleotide polymorphism; SNP; PCR primer;
diagnosis; ss.
Homo sapiens.
W09954500-A2.
28-OCT-1999.
21-APR-1999; 99WO-IB00822.
21-APR-1998; 98US-0082614.
23-NOV-1998; 98US-0109732.
(GEST) GENSET.
Cohen D, Blumenfeld M, Chumakov I;
WPI; 2000-013267/01.
Novel biallelic markers used to construct a high density disequilibrium
map of the human genome
Claim 8; Page 1528; 2745pp; English.
AAZ65654 to AAZ69578 represent human biallelic markers from the present
invention, which contain a polymorphic base at position 24 of their
nucleotide sequences. AAZ65654 to AAZ77440 represent amplification
primers for the biallelic markers. The biallelic markers of the
invention have a variety of uses: they can be used for high density
mapping of the human genome, and in complex association studies and
haplotyping studies which are useful in determining the genetic basis
for disease states. Compositions and methods of the invention can also
be useful for the identification of the targets for the development of
pharmaceutical agents and diagnostic methods, as well as the
characterisation of the differential efficacious responses to and side
effects from pharmaceutical agents acting on a disease as well as other
treatment.
N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
and 3367, are not actually given a sequence in the Sequence Listing
from the present invention.
Sequence 18 BP; 2 A; 2 C; 6 G; 8 T; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1566 TTTTACTGTTCTCA 1581
```

```

Db 1 TGTCTACTGTTCTCA 16
|||||
RESULT 604
AAA86605/C
ID AAA86605 standard; DNA; 18 BP.
XX
AC AAA86605;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cdc 2 kinase hammerhead ribozyme recognitoin site #36.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
restenosis; ss.
XX
OS Mammalia.
XX
PN W0200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US28772.
XX
PR 04-DEC-1998; 98US-0110954.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch RJ, Barber JR, Robbins JM;
XX
WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PCNA and Cyclin B1
XX
PS Example 1; Page 18; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAZ82415 to AAZ85787. The ribozyme of the invention is useful for
inhibiting restenosis by introduction of the ribozyme into cells.
CC The ribozyme is resistant to endonuclease activity and hence is
efficient in restenosis treatment.
XX
SQ Sequence 18 BP; 6 A; 2 C; 3 G; 7 T; 0 other;
Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1173 TTATTAGATAAATTTC 1188
|||||
DB 18 TTATTAGAGAAATTTC 3
|||||
RESULT 605
AAA86607/C
ID AAA86607 standard; DNA; 18 BP.
XX
AC AAA86607;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cdc 2 kinase hammerhead ribozyme recognitoin site #38.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
restenosis; ss.
XX
OS Mammalia.
```

XX WO200032765-A2.
XX 08-JUN-2000.
XX 06-DEC-1999; 99WO-US28772.
XX 04-DEC-1998; 98US-0110954.
XX (IMMU-) IMMUSOL INC.
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1
XX Example 1; Page 18; 109pp; English.
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells.
XX The ribozyme is resistant to endonuclease activity and hence is
XX efficient in restenosis treatment.
XX Sequence 18 BP; 7 A; 2 C; 2 G; 7 T; 0 other;
XX Query Match 1.0%; Score 12.8; DB 1; Length 18;
XX Best Local Similarity 87.5%; Pred. No. 4.5e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX 1172 TTTATTAGATAAATTT 1187
XX ||||| ||||| |||||
XX 16 TTTATTAGAGAAATTT 1
XX
XX RESULT 606
XX AAA86759/c
XX ID AAA86759 standard; DNA; 18 BP.
XX AA86759;
XX 04-DEC-2000 (first entry)
XX Cdc 2 kinase hammerhead ribozyme recognition site #190.
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
XX restenosis; ss.
XX Mammalia.
XX WO200032765-A2.
XX 08-JUN-2000.
XX 06-DEC-1999; 99WO-US28772.
XX 04-DEC-1998; 98US-0110954.
XX (IMMU-) IMMUSOL INC.
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1

XX Example 1; Page 23; 109pp; English.
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells.
XX The ribozyme is resistant to endonuclease activity and hence is
XX efficient in restenosis treatment.
XX Sequence 18 BP; 7 A; 3 C; 3 G; 5 T; 0 other;
XX Query Match 1.0%; Score 12.8; DB 1; Length 18;
XX Best Local Similarity 87.5%; Pred. No. 4.5e+02;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX 795 ATTTTGGCCATAAGTC 810
XX ||||| ||||| |||||
XX 18 ATTTTGGCCAGAAATTC 3
XX
XX RESULT 607
XX AAA10824/c
XX ID AAA10824 standard; DNA; 18 BP.
XX AA10824;
XX 14-JUL-2000 (first entry)
XX G-alpha-i1 antisense oligonucleotide ISIS# 25742.
XX G-alpha-i1; G protein; adenylyl cyclase hormonal inhibition; tumour;
XX plasma membrane regulation; antisense composition; treatment; prevent;
XX delay; infection; inflammation; tumour formation; research; diagnose; ss.
XX Synthetic.
XX US6046321-A.
XX 04-APR-2000.
XX 09-APR-1999; 99US-0289377.
XX 09-APR-1999; 99US-0289377.
XX (ISIS-) ISIS PHARM INC.
XX Cowser LM;
XX WPI; 2000-292434/25.
XX New antisense compounds targeting nucleic acids encoding human
XX G-alpha-i1 useful for modulating G-alpha-i1 expression and for treating
XX diseases associated with G-alpha-i1 expression
XX Claim 3; Column 38; 31pp; English.
XX Human G-alpha-i1 is a member of the Gi subfamily of G proteins which is
XX involved in hormonal inhibition of adenylyl cyclase and in the
XX regulation of plasma membrane enzymes. The expression of G-alpha-i1 is
XX altered in some tumours. The present sequence is a G-alpha-i1 antisense
XX oligonucleotide, which can be used to inhibit the expression of human
XX G-alpha-i1. The invention relates to antisense oligonucleotides
XX represented in AAA10814-A10853, which can be used in the treatment of
XX diseases or condition associated with the expression of G-alpha-i1 by
XX modulating the expression of G-alpha-i1 in cells or tissues. The
XX antisense compositions may also be used prophylactically, e.g. to
XX prevent or delay infection, inflammation, or tumour formation.
XX Furthermore, the antisense oligonucleotides may also be useful in
XX research and diagnostics, e.g. in detecting nucleic acids encoding
XX G-alpha-i1 by conjugation of an enzyme to the oligonucleotide, or

XX DE Cdc 2 kinase hammerhead ribozyme recognition site SEQ ID NO:4195.
 XX KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 XX KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 XX KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 XX KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 XX KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 XX KW antiproliferative; dermatological; anti-seborrheic; antidiabetic; virucide;
 XX KW anisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 XX KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 XX KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 XX KW sickle cell retinopathy; ss.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200130362-A2.
 XX PD 03-MAY-2001.
 XX PF 26-OCT-2000; 2000WO-US29500.
 XX PR 26-OCT-1999; 99US-0161532.
 XX PX (IMMU-) IMMUSOL INC.
 XX PI Robbins JM, Tritz R;
 XX DR WPI, 2001-300427/31.
 XX PT Treating proliferative skin or eye diseases and scarring, using
 XX PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
 XX PT matrix metalloproteinases, growth factors and cell-cycle dependent
 XX PT kinases -
 XX PS Disclosure; Page 378; 408pp; English.
 XX CC The present invention describes a method for treating a proliferative
 XX CC skin or eye disease and scarring. The method involves administering a
 XX CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 XX CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 XX CC dependent kinase, growth factor or a reductase, or administering a
 XX CC nucleic acid molecule (II) comprising a promoter operably linked to a
 XX CC dermatological, cytostatic, anti-seborrheic, antidiabetic, anisickling,
 XX CC ophthalmological, vulnary, keratolytic and virucide activities, and
 XX CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 XX CC in gene therapy. (I) and (II) are useful for treating proliferative
 XX CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 XX CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 XX CC also be used for treating proliferative eye diseases such as diabetic
 XX CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 XX CC prematurity and retinal detachment, and for treating and preventing
 XX CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 XX CC scar. AAH57577 to AAH62099 represent sequences used in the
 XX CC exemplification of the present invention.
 XX SX Sequence 18 BP; 5 A; 2 C; 3 G; 7 T; 0 other;
 XX SX Query Match 1.0%; Score 12.8; DB 1; Length 18;
 XX SX Best Local Similarity 87.5%; Pred. No. 4.5e+02;
 XX SX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1173 TTATTAGATAAATTTC 1188
 DB 18 TTATTAGATAAATTTC 3
 RESULT 611
 AAH61773/c
 ID AAH61773 standard; DNA; 18 BP.
 XX

AC AAH61773;
 XX 10-SEP-2001 (first entry)
 XX Cdc 2 kinase hammerhead ribozyme recognition site SEQ ID NO:4197.
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 XX KW recognition site; target; ribozyme binding site; eye disease; vulnary;
 XX KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 XX KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 XX KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 XX KW antiproliferative; dermatological; anti-seborrheic; antidiabetic; virucide;
 XX KW anisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 XX KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 XX KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 XX KW sickle cell retinopathy; ss.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200130362-A2.
 XX PD 03-MAY-2001.
 XX PF 26-OCT-2000; 2000WO-US29500.
 XX PR 26-OCT-1999; 99US-0161532.
 XX PX (IMMU-) IMMUSOL INC.
 XX PI Robbins JM, Tritz R;
 XX DR WPI, 2001-300427/31.
 XX PT Treating proliferative skin or eye diseases and scarring, using
 XX PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
 XX PT matrix metalloproteinases, growth factors and cell-cycle dependent
 XX PT kinases -
 XX PS Disclosure; Page 378; 408pp; English.
 XX CC The present invention describes a method for treating a proliferative
 XX CC skin or eye disease and scarring. The method involves administering a
 XX CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 XX CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 XX CC dependent kinase, growth factor or a reductase, or administering a
 XX CC nucleic acid molecule (II) comprising a promoter operably linked to a
 XX CC nucleic acid segment encoding (I). (I) can have antiproliferative,
 XX CC dermatological, cytostatic, anti-seborrheic, antidiabetic, anisickling,
 XX CC ophthalmological, vulnary, keratolytic and virucide activities, and
 XX CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 XX CC in gene therapy. (I) and (II) are useful for treating proliferative
 XX CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 XX CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 XX CC also be used for treating proliferative eye diseases such as diabetic
 XX CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 XX CC prematurity and retinal detachment, and for treating and preventing
 XX CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 XX CC scar. AAH57577 to AAH62099 represent sequences used in the
 XX CC exemplification of the present invention.
 XX SX Sequence 18 BP; 7 A; 2 C; 2 G; 7 T; 0 other;
 XX SX Query Match 1.0%; Score 12.8; DB 1; Length 18;
 XX SX Best Local Similarity 87.5%; Pred. No. 4.5e+02;
 XX SX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1172 TTATTAGATAAATTTC 1187
 DB 16 TTATTAGATAAATTTC 1
 RESULT 612

NA sequence and both leading and trailing PFS between (I) and the match, and determining value as result of previous step. The method can be used for determining a value indicative of a NA sequence being a transposon. The transposons identified by the method can be used to genotype a NA sequence using PCR (polymerase chain reaction) or hybridisation based protocols and sequences unique to the mixed transposons. The transposons can also be used in fingerprinting or linkage studies. Isolation of novel genes, producing mutated or knockout genes, and delivery of engineered genes. A copia-like retro transposon, PDR1, is successfully used to study polymorphisms. Miniature inverted-repeat transposable elements (MITEs) are used in a novel technology called inter-MITE polymorphism as mapping and fingerprinting tools in barley. The method is accurate, efficient, and allows high throughput identification of transposons compared to the use of standard genetic and molecular biological approaches. The transposon sequences discovered by the method greatly outnumber all of the plant transposon sequences previously reported. The present sequence represents a mined element RESite (related to empty site) oligonucleotide which is used in the exemplification of the present invention.

Sequence 18 BP; 7 A; 1 C; 2 G; 8 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 4.5e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1593 TATATAAGTAAATAG 1608

18 TATATAATCTAAATAG 3

RESULT 617

ABS54314

ABS54314 standard; DNA; 18 BP.

ABS54314;

05-DEC-2002 (first entry)

P. falciparum DHFR gene antisense oligonucleotide 281.

Anti-drug resistant infectious agent; resensitising drug resistance;

anti-infectious drug; drug resistant phenotype; Plasmodium; parasite;

anti-malarial drug resistance; mefloquine; quinine; chloroquine;

Pfmdr1 gene; protozoacide; dihydrofolate reductase-thymidylate synthase;

DHFR; ss.

Plasmodium falciparum.

Key Location/Qualifiers

modified_base 1..18

/tag= a

/mod_base= OTHER

/note= "OTHER= phosphorothioate internucleotide linkages"

US6440660-B1.

27-AUG-2002.

12-NOV-1996; 96US-0745485.

18-APR-1996; 96US-0634588.

17-NOV-1995; 95US-0560474.

(HYBR-) HYBRIDON INC.

(WORC-) WORCHESTER FOUND BIOMEDICAL RES.

Barker RH, Rapaport E, Zamecnik PC;

WPI; 2002-711526/77.

Resensitising drug-resistant infectious organism to anti-infectious organism drug, comprises use of synthetic oligonucleotide comprising a

PT sequence complementary to nucleic acid required for drug-resistant phenotype -

XX Examples; Column 21; 26pp; English.

XX The present invention relates to methods of resensitising an anti-drug resistant infectious agent to a drug. The method comprises culturing the infectious organism with antisense oligonucleotides with a sequence complementary to the nucleic acid required for drug resistance. The method is useful for resensitising drug resistant infectious organisms to anti-infectious drugs, thereby reversing the drug resistant phenotype of the organism. The method is useful for resensitising an anti-malarial drug resistant Plasmodium parasite to an anti-malarial drug, which involves culturing the parasite in the presence of an antisense oligonucleotide, to enable the oligonucleotide to hybridise to the nucleic acid, and contacting and culturing the parasite with an anti-malarial drug such as mefloquine, quinine, chloroquine or its derivatives, in the presence of the oligonucleotide. Preferably, the parasite is contacted and cultured with mefloquine or quinine. The antisense oligonucleotide is useful for down-regulating the expression of the pfmdr1 gene. By oligonucleotide reversing the expression of Pfmdr1 gene, the antisense oligonucleotide reverses the mefloquine-resistant phenotype of the parasite, thus restoring the parasite sensitivity to an important antimalarial drug. The method is useful for treating malaria. The method facilitates the continued use of mefloquine treatment in afflicted geographical areas, where otherwise, mefloquine use is increasingly restricted, due to decreased efficacy. Use of the antisense oligonucleotide allows a direct demonstration of the function of pfmdr1 gene in mefloquine resistance. The present sequence represents an antisense oligonucleotide directed towards the P. falciparum dihydrofolate reductase-thymidylate synthase (DHFR) gene in the examples of the present invention.

XX Sequence 18 BP; 7 A; 2 C; 2 G; 7 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 4.5e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1259 AAATAATTTTGTAGTA 1274

DB 2 AAATAATTTTCTGTA 17

RESULT 618

ABS54315/c

ID ABS54315 standard; DNA; 18 BP.

XX ABS54315;

AC ABS54315;

DT 05-DEC-2002 (first entry)

XX P. falciparum DHFR gene antisense oligonucleotide 282.

Anti-drug resistant infectious agent; resensitising drug resistance;

anti-infectious drug; drug resistant phenotype; Plasmodium; parasite;

anti-malarial drug resistance; mefloquine; quinine; chloroquine;

Pfmdr1 gene; protozoacide; dihydrofolate reductase-thymidylate synthase;

DHFR; ss.

Plasmodium falciparum.

Key Location/Qualifiers

modified_base 1..18

/tag= a

/mod_base= OTHER

/note= "OTHER= phosphorothioate internucleotide linkages"

US6440660-B1.

27-AUG-2002.

12-NOV-1996; 96US-0745485.
 18-APR-1996; 96US-0634588.
 17-NOV-1995; 95US-0560474.
 (HYBR-) HYBRIDON INC.
 (WORC-) WORCHESTER FOUND BIOMEDICAL RES.
 Barker RH, Rapaport E, Zamecnik PC;
 WPI; 2002-711526/77.
 Resensitising drug-resistant infectious organism to anti-infectious
 organism drug, comprises use of synthetic oligonucleotide comprising a
 sequence complementary to nucleic acid required for drug-resistant
 phenotype -
 Examples; Column 21; 26pp; English.
 The present invention relates to methods of resensitising an
 anti-drug resistant infectious agent to a drug. The method
 comprises culturing the infectious organism with antisense
 oligonucleotides with a sequence complementary to the nucleic acid
 required for drug resistance. The method is useful for resensitising
 drug resistant infectious organisms to anti-infectious drugs,
 thereby reversing the drug resistant phenotype of the organism. The
 method is useful for resensitising an anti-malarial drug resistant
 Plasmodium parasite to an anti-malarial drug, which involves culturing
 the parasite in the presence of an antisense oligonucleotide, to
 enable the oligonucleotide to hybridise to the nucleic acid and
 as mefloquine, quinine, chloroquine or its derivatives, in the presence
 of the oligonucleotide. Preferably, the parasite is contacted and
 cultured with mefloquine or quinine. The antisense oligonucleotide is
 useful for down-regulating the expression of the pfmdr1 gene. By
 down-regulating the expression of pfmdr1 gene, the antisense
 oligonucleotide reverses the mefloquine-resistant phenotype of the
 parasites, thus restoring the parasite sensitivity to an important
 antimalarial drug. The method is useful for treating malaria. The
 method facilitates the continued use of mefloquine treatment in
 afflicted geographical areas, where otherwise, mefloquine use is
 increasingly restricted, due to decreased efficacy. Use of the
 antisense oligonucleotide allows a direct demonstration of the
 function of pfmdr1 gene in mefloquine resistance. The present
 sequence represents an antisense oligonucleotide directed
 towards the P. falciparum dihydrofolate reductase-thymidylate
 synthase (DHFR) gene in the examples of the present invention.
 Note: This sequence appears as the second SEQ ID No 15 in column 21
 of the specification and as SEQ ID No 15 in the sequence listing.
 Query Match 1.0%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 4.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1259 AAATAATTTTCTAGTA 1274
 17 AAATAATTTCTTCGTA 2
 RESULT 619
 ABQ65395
 ID ABQ65395 standard; DNA; 18 BP.
 AC ABQ65395;
 DT 20-AUG-2002 (first entry)
 DE Human gene methylation status determination oligo SEQ ID NO: 7.
 Toxicological diagnosis; DNA methylation; methylation status;

toxic response; human; ds.
 Homo sapiens.
 WO200240710-A2.
 23-MAY-2002.
 08-NOV-2001; 2001WO-EPI12951.
 14-NOV-2000; 2000DE-1056802.
 (EPIG-) EPIGENOMICS AG.
 Olek A, Piepenbrock C, Berlin K;
 WPI; 2002-463571/49.
 Toxicological diagnosis, useful for diagnosis and prognosis of adverse
 reactions, based on effect of test compounds on methylation status of
 selected genes, involves determining changes in DNA methylation status
 Example 3; Page 107; 113pp; German.
 The present invention relates to a method of toxicological diagnosis
 involving taking a DNA-containing sample from an organism or cell culture
 that has been treated with a test compound and determining any changes in
 the DNA methylation status or pattern caused by said test compound. The
 method is used for diagnosis and prognosis of adverse toxic responses in
 individuals. The present sequence is a human sequence used to demonstrate
 the method of the invention.
 Sequence 18 BP; 2 A; 0 C; 4 G; 12 T; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 4.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1143 TTTATTTTATTTTAGA 1158
 2 TTTTGTGTTTAGA 17
 RESULT 620
 ABK34044
 ID ABK34044 standard; DNA; 18 BP.
 AC ABK34044;
 DT 18-JUN-2002 (first entry)
 DE Human NP1 probe #2.
 Human; ss; astrocytoma; cytostatic; staging; cysteine methylation; CpG;
 bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry;
 matrix assisted laser desorption/ionization mass spectrometry; probe.
 Homo sapiens.
 WO200202808-A2.
 10-JAN-2002.
 02-JUL-2001; 2001WO-EP07538.
 30-JUN-2000; 2000DE-1032529.
 01-SEP-2000; 2000DE-1043826.
 (EPIG-) EPIGENOMICS AG.
 Olek A, Piepenbrock C, Berlin K;

WPI; 2002-171649/22.

Novel chemically modified genomic DNA sequences, useful in the characterisation, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas or predisposition to astrocytomas.

Example 2; Page 18; 37pp; English.

The invention relates to a nucleic acid comprising a sequence (I) of at least 18 bases in length of a segment of chemically pre-treated genomic DNA which has any one of the sequences of (ABK33919-ABK34032) or its complement. Also included are an oligonucleotide or peptide nucleic acid (or set thereof) of at least 9 nucleotides which hybridises to (I), primers for (I), probes for detecting cytosine methylation or single-nucleotide polymorphisms (SNP) in (I), an array of oligomers or peptide nucleic acids for analysing diseases associated with the methylation states of the CpG dinucleotides of (I). The array is useful for determining genetic and/or epigenetic parameters, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas, or the predisposition to astrocytomas by analysing cytosine methylation, involves obtaining a biological sample containing genomic DNA, extracting the genomic DNA, converting cytosine bases which are unmethylated at the 5-position, in the genomic DNA sample, to uracil or another base which is dissimilar to cytosine in terms of hybridisation behaviour, by chemical treatment and amplifying chemically pre-treated genomic DNA fragments using the array and a polymerase, where the amplificates carry a detectable label. The method further involves identifying methylation status of one or more cytosine positions, and analysing methylation status of the cytosine positions by reference to one or more data sets. The genomic DNA is chemically treated by using a bisulphite, hydrogen sulphite or disulphite. The amplification step amplifies DNA which is of particular interest in astrocytoma or brain tissue, based on the specific genomic methylation status of brain tissues, as opposed to background DNA. The amplificates carry a fluorescent label or radioactive label. Optionally, the labels of the amplificates are detachable molecule fragments having a typical mass which are detected in a mass spectrometer. The fragments of chemically pre-treated genomic DNA to be amplified, have a single positive or negative charge for a better detectability in the mass spectrometer. Preferably, the amplificates or fragments of the amplificates are detected by matrix assisted laser desorption/ionization mass spectrometry (MALDI) or using electron spray mass spectrometry (ESI). The present sequence is a probe used to detect a region containing a methylated cytosine from one of the chemically pre-treated reference DNA samples of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 18 BP; 11 A; 4 C; 0 G; 3 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1400 ATTAACACAGCCAAA 1415
|||||
2 ATTAACACAGCCAAA 17

RESULT 621
ABK40096/c

ABK40096 standard; DNA; 18 BP.

ABK40096;

21-MAY-2002 (first entry)

Human super oxide dismutase 1 oligonucleotide probe #2.

Human; ss; bisulphite treatment; CpG; DNA methylation; cancer; tumour;

KW

cytostatic; ALDH6; CYP11A; CYP11B; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism; probe; superoxide dismutase 1.

OS Homo sapiens.

XX WO200202806-A2.

PN 10-JAN-2002.

XX 29-JUN-2001; 2001WO-EP07470.

XX 30-JUN-2000; 2000DE-1032529.

PR 01-SEP-2000; 2000DE-1043826.

XX (SPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-154757/20.

New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer

Example 1; Page 16; 24pp; English.

The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the genes ALDH6 (NM_006931), CYP11A (NM_000781), CYP11B1 (NM_000497), CYP3A3 (NM_000776 and NM_017460), DPYD (NM_000110), EPHX2 (NM_001979), OCLN (NM_002538), TXNRD1 (NM_003330), UGT8 (NM_003360), MRP (NM_004996), NM_019900, NM_019901, NM_019902, NM_019862, NM_019898, NM_019899 and their complementary sequences, or a sequence (SI) chosen from 87 sequences and their complements. The chemical pretreatment is bisulphite treatment to convert cytosines (but not methyl-cytosines) into uracils. Also included are an oligomer (II) in particular an oligonucleotide or a peptide nucleic acid (PNA)-oligomer, comprising in each case at least one base sequence having a length of 9 nucleotides which hybridises to or is identical to a chemically pretreated DNA of genes associated with pharmacogenomics and their complements, arranged in an array for analysing diseases associated with the methylation state (CpG) and/or detecting SNPs (single nucleotide polymorphisms) of the 87 sequences. The oligomers may also be used as PCR primers. The set of 87 nucleic acids and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence is a capture probe which captures a 451bp fragment of the human superoxide dismutase gene which has been treated with bisulphite to convert cytosines to uracils. The fragment is only captured if a methylated cytosine is present at position 111.

Sequence 18 BP; 2 A; 0 C; 5 G; 11 T; 0 other;

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1400 ATTAACACAGCCAAA 1415
|||||
DB 17 ATTAACACAGCCAAA 2

RESULT 622

ABA83553

ID ABA83553 standard; DNA; 18 BP.

XX ABA83553;

AC ABA83553;

XX 08-FEB-2002 (first entry)

XX Mouse WP-1 antisense oligonucleotide SEQ ID NO 96.

Human; mouse; rat; antisense gene therapy; MP-1; MAP kinase Partner 1;
 antiinflammatory; cytostatic; antimicrobial; infection; tumour;
 phosphorothioate; ss.
 Mus musculus.
 Synthetic.

Key Location/Qualifiers
 modified_base 1..18
 /tag= a
 /mod_base= OTHER
 /note= "phosphorothioate backbone linkage, all cytidine
 residues are 5-methylcytidines"

modified_base 1..4
 /tag= b
 /mod_base= OTHER
 /note= "2'-MOE wings"

modified_base 15..18
 /tag= c
 /mod_base= OTHER
 /note= "2'-MOE wings"

US6306606-B1.
 23-OCT-2001.
 22-NOV-2000; 2000US-0721822.
 22-NOV-2000; 2000US-0721822.
 (ISIS-) ISIS PHARM INC.
 (UTVI-) UNIV VIRGINIA.

Weber MJ, Wyatt J, Cowser LM;
 WPI; 2002-040199/05.
 New antisense oligonucleotides for modulating the expression of MP-1
 (MAP kinase partner 1), for preventing, delaying or treating infection,
 inflammation or tumour formation, especially in humans

Claim 1; Column 43-44; 47pp; English.

The invention relates to an antisense compound (ABA83459-ABA83576) which
 is up to 30 nucleobases in length and that inhibits the expression of
 MP-1 (MAP kinase Partner 1) in cells or tissues comprising contacting the
 cells or tissues in vitro with the antisense compound so that expression
 of MP-1 is inhibited. The antisense compounds have potential
 antiinflammatory, cytostatic and antimicrobial activity. The antisense
 compounds are useful for diagnostics, therapeutics, prophylaxis or as
 research reagents or kits. The antisense oligonucleotides are useful in
 gene therapy for treating an animal, particularly a human, suspected of
 having or being prone to a disease or condition associated with the
 expression of MP-1. In particular, the antisense oligonucleotides are
 useful for preventing, delaying or treating infection, inflammation or
 tumour formation. The present sequence is that of a mouse MP-1 antisense
 oligonucleotide, comprising a chimeric oligonucleotide gapmer 18
 nucleotides in length, composed of a central gap region of ten
 2'-deoxynucleotides flanked by four nucleotide 2'-MOE wings.

Query Match 1.0%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 4.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1353 CTGCTGTTGGTAGTCT 1368
 |||||
 DB 3 CTGCTGTTGGTAGTCT 18

RESULT 623
 ABZ70969

ID ABZ70969 standard; RNA; 18 BP.
 AC ABZ70969;
 XX
 DT 24-APR-2003 (first entry)
 XX
 DE Human bcl-2 related mRNA sequence #2.
 XX
 KW Nervous tumour; Hu protein; cytostatic; gene therapy; neuroblastoma;
 human; bcl-2; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200294306-A1.
 FN
 XX 28-NOV-2002.
 PD
 XX 03-OCT-2001; 2001WO-JP08701.
 PF
 XX 24-MAY-2001; 2001JP-0155237.
 PR
 XX (NTSC-) JAPAN SCI & TECHNOLOGY CORP.
 PA
 XX Okano H, Akamatsu W;
 PI
 XX WPI; 2003-093385/08.
 DR
 XX Remedies for nervous tumor containing Hu protein, its variant or their
 encoded gene as active ingredient, applicable in novel method for
 treating neuroblastoma
 PT
 XX Example 4; Fig 7; 20pp; Japanese.
 PS
 XX The present invention describes a method for the treatment of nervous
 CC tumours which comprises as active ingredients: (1) Hu protein; or
 CC (2) a polypeptide based on the protein but with some amino acids
 CC substituted, deleted, added or inserted; or (3) the gene encoding
 CC Hu protein. Hu protein has cytostatic activity and can be used in
 CC gene therapy. The method is used for treating nervous tumour
 CC (preferably neuroblastoma). The present sequence represents a human
 CC bcl-2 related RNA sequence, which is used in an example from the
 CC present invention.
 CC
 XX Sequence 18 BP; 6 A; 1 C; 2 G; 2 T; 7 U; 0 other;
 SQ
 Query Match 1.0%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 50.0%; Pred. No. 4.5e+02;
 Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1050 ATGTATTATTATTAAGC 1065
 |||||
 DB 2 AAGTAUUUUUUUUAAGC 17

RESULT 624
 ABZ10410
 ID ABZ10410 standard; DNA; 18 BP.
 XX
 AC ABZ10410;
 XX
 DT 16-JAN-2003 (first entry)
 XX
 DE Haematopoietic cell proliferation disorder related oligonucleotide #550.
 DE
 XX Human; haematopoietic cell proliferation disorder; cytostatic;
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KW cytosine methylation state; probe; primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX Synthetic.
 OS
 XX WO200277272-A2.
 PN
 XX

S Synthetic.
 X WO200277272-A2.
 N
 X
 D 03-OCT-2002.
 X
 F 26-MAR-2002; 2002WO-EP03401.
 X
 X 26-MAR-2001; 2001US-278333P.
 X
 X (EPIG-) EPIGENOMICS AG.
 X
 X Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 I Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
 I Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T;
 I Pelet C, Schwöpe I, Ziebarth H;
 X WPI; 2003-018942/01.
 X
 T Detecting and differentiating between hematopoietic cell proliferative
 disorders, comprises contacting a target nucleic acid with a reagent
 T that distinguishes between methylated and non-methylated CpG
 T dinucleotides -
 X
 S Claim 15; Page 52; 117pp; English.
 X
 C The present invention describes a method for detecting and
 C differentiating between hematopoietic cell proliferative disorders
 C associated with at least 1 gene and/or their regulatory regions in a
 C subject. The method comprises contacting a target nucleic acid in a
 C biological sample obtained from the subject with at least 1 reagent,
 C which distinguishes between methylated and non-methylated CpG
 C dinucleotides within the target nucleic acid. AB209861 to AB211118
 C represent specifically claimed nucleotide sequences from the present
 C invention. Oligonucleotides from the present invention can be used: for
 C differentiating between healthy hematopoietic cells and proliferative
 C disorder hematopoietic cells; for differentiating between acute
 C lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 C determining the cytosine methylation state and/or single nucleotide
 C polymorphisms (SNPs) of hematopoietic cell proliferation disorder
 C related sequences and their complements; and as primers for the
 C amplification of hematopoietic cell proliferation disorder related
 C DNA sequences. The nucleotide sequences from the present invention can
 C also be used for detecting a predisposition to, differentiation between
 C subclasses, diagnosis, prognosis, treatment and/or monitoring of
 C hematopoietic cell proliferative disorders. The present method enables
 C a highly specific classification of hematopoietic cell proliferative
 C disorders allowing for improved and informed treatment of patients.
 X
 G Sequence 18 BP; 3 A; 0 C; 4 G; 11 T; 0 other;
 SQ Query Match 1.0%; Score 12.6; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 4.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 2Y 611 AATCTACAAAAACAA 626
 |||||
 Db 16 AATTCGAAAAACAA 1
 |||||
 RESULT 627
 ABZ10922
 ID ABZ10922 standard; DNA; 18 BP.
 XX
 AC ABZ10922;
 XX
 DT 16-JAN-2003 (first entry)
 XX
 DE Hematopoietic cell proliferation disorder related oligonucleotide #1062.
 XX
 KW Human; hematopoietic cell proliferation disorder; cytostatic;
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KW cytosine methylation state; probe; primer; ss.

XX Homo sapiens.
 OS Synthetic.
 XX WO200277272-A2.
 XX
 XX 03-OCT-2002.
 XX
 PD 26-MAR-2002; 2002WO-EP03401.
 XX
 XX 26-MAR-2001; 2001US-278333P.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
 PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T;
 PI Pelet C, Schwöpe I, Ziebarth H;
 XX WPI; 2003-018942/01.
 DR
 XX Detecting and differentiating between hematopoietic cell proliferative
 XX disorders, comprises contacting a target nucleic acid with a reagent
 XX that distinguishes between methylated and non-methylated CpG
 XX dinucleotides -
 XX
 PS Claim 15; Page 70; 117pp; English.
 XX
 C The present invention describes a method for detecting and
 C differentiating between hematopoietic cell proliferative disorders
 C associated with at least 1 gene and/or their regulatory regions in a
 C subject. The method comprises contacting a target nucleic acid in a
 C biological sample obtained from the subject with at least 1 reagent,
 C which distinguishes between methylated and non-methylated CpG
 C dinucleotides within the target nucleic acid. AB209861 to AB211118
 C represent specifically claimed nucleotide sequences from the present
 C invention. Oligonucleotides from the present invention can be used: for
 C differentiating between healthy hematopoietic cells and proliferative
 C disorder hematopoietic cells; for differentiating between acute
 C lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 C determining the cytosine methylation state and/or single nucleotide
 C polymorphisms (SNPs) of hematopoietic cell proliferation disorder
 C related sequences and their complements; and as primers for the
 C amplification of hematopoietic cell proliferation disorder related
 C DNA sequences. The nucleotide sequences from the present invention can
 C also be used for detecting a predisposition to, differentiation between
 C subclasses, diagnosis, prognosis, treatment and/or monitoring of
 C hematopoietic cell proliferative disorders. The present method enables
 C a highly specific classification of hematopoietic cell proliferative
 C disorders allowing for improved and informed treatment of patients.
 XX
 SQ Sequence 18 BP; 4 A; 1 C; 1 G; 12 T; 0 other;
 Query Match 1.0%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 4.5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 833 TTTTTCCTGTTAAAT 848
 |||||
 Db 1 TTTTTCCTGTTAAAT 16
 |||||
 RESULT 628
 AAA83135/C
 ID AAA83135 standard; DNA; 19 BP.
 XX
 AC AAA83135;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE cdk7 ribozyme binding site #56.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;

XI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 TT designed to detect single nucleotide polymorphisms and cytosine
 TT methylation status -
 XX Claim 1; SEQ ID 5459; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation.
 XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 XX AB100010-AB182073 represent the oligomers described in the invention.
 XX NOTE: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 3 A; 0 C; 2 G; 7 T; 1 other;
 Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 YY 1535 TTTAAGATGTTT 1547
 YY |||||
 YY 1 TTTAAGATGTTT 13
 RESULT 631
 LBC05469/C
 ID ABC05469 standard; DNA; 13 BP.
 XX ABC05469;
 XX 20-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 5460 for detecting SNP TSC0001825.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single nucleotide polymorphisms and cytosine
 XX methylation status -
 XX Claim 1; SEQ ID 5460; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC AB100010-AB182073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 7 A; 2 C; 0 G; 3 T; 1 other;
 Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1535 TTTAAGATGTTT 1547
 QY |||||
 QY 13 TTTAAGATGTTT 1
 Db 13 TTTAAGATGTTT 1
 RESULT 632
 ABC12854
 ID ABC12854 standard; DNA; 13 BP.
 XX ABC12854;
 XX 20-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 12861 for detecting SNP TSC0003005.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single nucleotide polymorphisms and cytosine
 XX methylation status -
 XX Claim 1; SEQ ID 12861; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation.
 XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 XX AB100010-AB182073 represent the oligomers described in the invention.
 XX NOTE: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 5 A; 0 C; 0 G; 7 T; 1 other;
 Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Query Match 1.0%; Score 12.6; DB 1; Length 13;


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18-OCT-2001.
XX 06-APR-2001; 2001WO-IB00713.
XX 07-APR-2000; 2000DE-1019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX Claim 1; SEQ ID 13836; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABI00010-ABI92073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 13 BP; 6 A; 0 C; 1 G; 5 T; 1 other;
XX Query Match 1.0%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.7e+02;
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1618 AAATATAATTGT 1630
XX 1 AAATATAATTGT 13
XX
XX RESULT 637
XX ABC23681/c
XX ID ABC23681 standard; DNA; 13 BP.
XX AC ABC23681;
XX XX 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 23698 for detecting SNP TSC0005244.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX XX 18-OCT-2001.
XX XX 06-APR-2001; 2001WO-IB00713.
XX XX 07-APR-2000; 2000DE-1019173.
XX XX (EPIG-) EPIGENOMICS AG.
XX XX Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX Claim 1; SEQ ID 23698; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABI00010-ABI92073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 13 BP; 10 A; 2 C; 0 G; 0 U; 1 other;
XX Query Match 1.0%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.7e+02;
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 618 AAAAACACAA 630
XX 1 AAAAACACAA 13
XX
XX RESULT 636
XX ABC23680
XX ID ABC23680 standard; DNA; 13 BP.
XX AC ABC23680;
XX XX 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 23697 for detecting SNP TSC0005244.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX XX 18-OCT-2001.
XX XX 06-APR-2001; 2001WO-IB00713.
XX XX 07-APR-2000; 2000DE-1019173.
XX XX (EPIG-) EPIGENOMICS AG.
XX XX Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is

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AB100010-AB182073 represent the oligomers described in the invention.
 NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 5 A; 1 C; 0 G; 6 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1618 AATATTAATTGT 1630
 |||||
 13 AATATTAATTGT 1

SULT 638
 C26934
 ABC26934 standard; DNA; 13 BP.

ABC26934;
 20-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 26951 for detecting SNP TSC0007310.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.
 18-OCT-2001.

06-APR-2001; 2001WO-IB00713.
 07-APR-2000; 2000DE-1019173.
 (EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;
 WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 26951; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

AB100010-AB182073 represent the oligomers described in the invention.
 NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 2 A; 0 C; 0 G; 10 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1143 TTTATTTTATTT 1155
 |||||

Db 1 TTTATTTTATTT 13

RESULT 639
 ABC26935/c
 ID ABC26935 standard; DNA; 13 BP.

XX ABC26935;
 XX 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 26952 for detecting SNP TSC0007310.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.
 XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

XX Claim 1; SEQ ID 26952; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

XX AB100010-AB182073 represent the oligomers described in the invention.
 XX NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 10 A; 0 C; 0 G; 2 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1143 TTTATTTTATTT 1155
 |||||
 Db 13 TTTATTTTATTT 1

RESULT 640
 ABC45016/c
 ID ABC45016 standard; DNA; 13 BP.

XX ABC45016;
 XX 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 45033 for detecting SNP TSC0013165.

W SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 W peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 W central nervous system; gastrointestinal; respiratory; immune; metabolic.
 X Homo sapiens.
 X WO200177384-A2.
 X 18-OCT-2001.
 X 06-APR-2001; 2001WO-IB00713.
 X 07-APR-2000; 2000DE-1019173.
 X (EPIG-) EPIGENOMICS AG.
 X Olek A, Piepenbrock C, Berlin K;
 X WPI; 2001-657177/75.
 X Set of oligonucleotides, useful for diagnosis and cell typing, is
 X designed to detect single nucleotide polymorphisms and cytosine
 X methylation status -
 X Claim 1; SEQ ID 45033; 29pp + Sequence Listing; German.
 X This invention describes novel oligonucleotide primers or peptide nucleic
 X acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 X and cytosine methylation status in chemically pretreated genomic DNA. The
 X oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 X range of diseases including immune system, gastrointestinal, respiratory,
 X central nervous system, cardiovascular and metabolic disorders. The
 X oligomers are also used for detecting cell type differentiation.
 X ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 X ABI00010-ABI82073 represent the oligomers described in the invention.
 X NOTE: The sequence data for this patent did not form part of the printed
 X specification, but was obtained in electronic format from WIPO at
 X ftp.wipo.int/pub/published_pct_sequences.
 X Sequence 13 BP; 0 A; 0 C; 3 G; 9 T; 1 other;
 X Query Match 1.0%; Score 12.6; DB 1; Length 13;
 X Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 X Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 X 1208 AACAAACAACAA 1220
 X :|||||
 X 13 RACAAACAACAA 1
 X RESULT 641
 X ABC45017
 X ID ABC45017 standard; DNA; 13 BP.
 X AC ABC45017;
 X DT 21-FEB-2002 (first entry)
 X DE Oligonucleotide SEQ ID NO 45034 for detecting SNP TSC0013165.
 X SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 X peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 X central nervous system; gastrointestinal; respiratory; immune; metabolic.
 X Homo sapiens.
 X WO200177384-A2.
 X 18-OCT-2001.
 X 06-APR-2001; 2001WO-IB00713.
 X 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single nucleotide polymorphisms and cytosine
 XX methylation status -
 XX Claim 1; SEQ ID 45034; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation.
 XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 XX ABI00010-ABI82073 represent the oligomers described in the invention.
 XX NOTE: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 9 A; 3 C; 0 G; 0 U; 1 other;
 XX Query Match 1.0%; Score 12.6; DB 1; Length 13;
 XX Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1208 AACAAACAACAA 1220
 XX :|||||
 XX Db 1 RACAAACAACAA 13
 XX RESULT 642
 XX ABC52710
 XX ID ABC52710 standard; DNA; 13 BP.
 XX AC ABC52710;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 52727 for detecting SNP TSC0014602.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single nucleotide polymorphisms and cytosine
 XX methylation status -
 XX Claim 1; SEQ ID 52727; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. AB00010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB10010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 4 A; 0 C; 1 G; 7 T; 1 other;
Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

596 AGTATTATTATT 608
1 AGTATTATTATT 13

RESULT 643
ABC52711/c
ABC52711 standard; DNA; 13 BP.

ABC52711;

21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 52728 for detecting SNP TSC0014602.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status -

Claim 1; SEQ ID 52728; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB10010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 7 A; 1 C; 0 G; 4 T; 1 other;
Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

596 AGTATTATTATT 608
13 AGTATTATTATT 1

RESULT 644

ABC59940

ID ABC59940 standard; DNA; 13 BP.

ABC59940;

21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 59957 for detecting SNP TSC0016027.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status -

Claim 1; SEQ ID 59957; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and AB10010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 3 A; 0 C; 2 G; 7 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1169 TGTATTATTAGAT 1181
1 TGTATTATTAGAY 13

RESULT 645
ABC59941/c

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status -

Claim 1; SEQ ID 72784; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

ABT00010-ABT02073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 7 A; 1 C; 0 G; 4 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 3.7e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1609 AACATTAAAAAT 1621

:|||||
1 AACATTAAAAAT 13

SULT 648

C75212/c

ABC75212 standard; DNA; 13 BP.

ABC75212;

21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 75229 for detecting SNP TSC0019311.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status -

Claim 1; SEQ ID 75229; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABI00010-ABI182073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 13 BP; 3 A; 0 C; 2 G; 7 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 3.7e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 999 ATCATACATAAA 1011

Db :|||||
13 RTCATACATAAA 1

RESULT 649

ABC75213

ID ABC75213 standard; DNA; 13 BP.

XX AC ABC75213;

XX

DT 21-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 75230 for detecting SNP TSC0019311.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

FN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB00713.

XX

PR 07-APR-2000; 2000DE-1019173.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

WPI; 2001-657177/75.

DR

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine

PT

PT

PT

XX

PS Claim 1; SEQ ID 75230; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABT00010-ABT02073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 13 BP; 7 A; 2 C; 0 G; 3 T; 1 other;

Query Match

Best Local Similarity 1.0%; Score 12.6; DB 1; Length 13;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

Y 999 ATCATAACATAAA 1011
b :|||||
1 RTCTACATAAA 13

RESULT 650
BC80810/c
D ABC80810 standard; DNA; 13 BP.
K
K ABC80810;
K
K 21-FEB-2002 (first entry)
T
X
E Oligonucleotide SEQ ID NO 80827 for detecting SNP TSC0020471.
X
W SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
W peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
W central nervous system; gastrointestinal; respiratory; immune; metabolic.
X
S Homo sapiens.
S
N WO200177384-A2.
N
X 18-OCT-2001.
D
X
F 06-APR-2001; 2001WO-IB00713.
X
F 07-APR-2000; 2000DE-1019173.
R
X (EPIG-) EPIGENOMICS AG.
X
X Olek A, Piepenbrock C, Berlin K;
I
X WPI; 2001-657177/75.
R
X Set of oligonucleotides, useful for diagnosis and cell typing, is
T designed to detect single nucleotide polymorphisms and cytosine
T methylation status -
T
S Claim 1; SEQ ID 80827; 29pp + Sequence Listing; German.
S
C This invention describes novel oligonucleotide primers or peptide nucleic
C acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
C and cytosine methylation status in chemically pretreated genomic DNA. The
C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
C range of diseases including immune system, gastrointestinal, respiratory,
C central nervous system, cardiovascular and metabolic disorders. The
C oligomers are also used for detecting cell type differentiation.
C ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
C ABI00010-ABI82073 represent the oligomers described in the invention.
C NOTE: The sequence data for this patent did not form part of the printed
C specification, but was obtained in electronic format from WIPO at
C ftp.wipo.int/pub/published_pct_sequences.
X
Q Sequence 13 BP; 2 A; 0 C; 3 G; 7 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 612 ATCTACAAAAAAC 624
b :|||||
13 RTCTACAAAAAAC 1

RESULT 651
BC80811
D ABC80811 standard; DNA; 13 BP.
X
X ABC80811;
X
X 21-FEB-2002 (first entry)
T

```

```

XX Oligonucleotide SEQ ID NO 80828 for detecting SNP TSC0020471.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
FN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB00713.
PP
XX
XX 07-APR-2000; 2000DE-1019173.
PR
XX (SPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
PT
XX
XX Claim 1; SEQ ID 80828; 29pp + Sequence Listing; German.
PS
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 7 A; 3 C; 0 G; 2 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 612 ATCTACAAAAAAC 624
Db :|||||
1 RTCTACAAAAAAC 13

RESULT 652
ABC93680/c
ID ABC93680 standard; DNA; 13 BP.
XX
XX ABC93680;
AC
XX
XX 21-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 93697 for detecting SNP TSC0023406.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
FN
XX
XX 18-OCT-2001.
PD
XX

```


06-APR-2001; 2001WO-IB00713.
 07-APR-2000; 2000DE-1019173.
 (EPIG-) EPIGENOMICS AG.
 Olek A, Piepenbrock C, Berlin K;
 WPI; 2001-657177/75.
 Set of oligonucleotides, useful for diagnosis and cell typing, is
 designed to detect single nucleotide polymorphisms and cytosine
 methylation status -
 Claim 1; SEQ ID 93697; 29pp + Sequence Listing; German.
 This invention describes novel oligonucleotide primers or peptide nucleic
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 and cytosine methylation status in chemically pretreated genomic DNA. The
 oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 range of diseases including immune system, gastrointestinal, respiratory,
 central nervous system, cardiovascular and metabolic disorders. The
 oligomers are also used for detecting cell type differentiation.
 ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 ABI00010-ABI82073 represent the oligomers described in the invention.
 NOTE: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format from WIPO at
 ftp.wipo.int/pub/published_pct_sequences.
 Sequence 13 BP; 1 A; 0 C; 2 G; 9 T; 1 other;
 Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 619 AAAAACAACAAT 631
 :|||||
 13 AAAAACAACAAT 1
 RESULT 653
 C93681
 ABC93681 standard; DNA; 13 BP.
 ABC93681;
 21-FEB-2002 (first entry)
 Oligonucleotide SEQ ID NO 93698 for detecting SNP TSC0023406.
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 central nervous system; gastrointestinal; respiratory; immune; metabolic.
 Homo sapiens.
 WO200177384-A2.
 18-OCT-2001.
 06-APR-2001; 2001WO-IB00713.
 07-APR-2000; 2000DE-1019173.
 (EPIG-) EPIGENOMICS AG.
 Olek A, Piepenbrock C, Berlin K;
 WPI; 2001-657177/75.
 Set of oligonucleotides, useful for diagnosis and cell typing, is
 designed to detect single nucleotide polymorphisms and cytosine
 methylation status -

XX Claim 1; SEQ ID 93698; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 13 BP; 9 A; 2 C; 0 G; 1 T; 1 other;
 Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 619 AAAAACAACAAT 631
 DB 1 AAAAACAACAAT 13
 RESULT 654
 ABC95530/c
 ID ABC95530 standard; DNA; 13 BP.
 XX
 AC ABC95530;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 95547 for detecting SNP TSC0023777.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PP 06-APR-2001; 2001WO-IB00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 DR
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX
 XX
 PS Claim 1; SEQ ID 95547; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

Q Sequence 13 BP; 1 A; 0 C; 2 G; 9 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 1249 GATAAACAACAAA 1261

b 13 RATAAACAACAAA 1

RESULT 655

ABC95531
ID ABC95531 standard; DNA; 13 BP.

AC ABC95531;

XX 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 95548 for detecting SNP TSC0023777.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single nucleotide polymorphisms and cytosine
methylation status -

Claim 1; SEQ ID 95548; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and

CC ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 9 A; 2 C; 0 G; 1 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1249 GATAAACAACAAA 1261

DB 1 RATAAACAACAAA 13

RESULT 656

ABF24642
ID ABF24642 standard; DNA; 13 BP.

XX ABF24642;

XX 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 124639 for detecting SNP TSC0031166.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single nucleotide polymorphisms and cytosine
methylation status -

Claim 1; SEQ ID 124639; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and

CC ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 4 A; 0 C; 1 G; 7 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1043 ATTATTATGATAT 1055

DB 1 ATTATTATGATAT 13

RESULT 657

ABF24643/C
ID ABF24643 standard; DNA; 13 BP.

XX ABF24643;

XX 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 124640 for detecting SNP TSC0031166.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

4 central nervous system; gastrointestinal; respiratory; immune; metabolic.
 5 Homo sapiens.
 6 WO200177384-A2.
 7 18-OCT-2001.
 8 06-APR-2001; 2001WO-IB00713.
 9 07-APR-2000; 2000DE-1019173.
 10 (EPIG-) EPIGENOMICS AG.
 11 Olek A, Piepenbrock C, Berlin K;
 12 WPI; 2001-657177/75.
 13 Set of oligonucleotides, useful for diagnosis and cell typing, is
 14 designed to detect single nucleotide polymorphisms and cytosine
 15 methylation status -
 16 Claim 1; SEQ ID 124640; 29pp + Sequence Listing; German.
 17 This invention describes novel oligonucleotide primers or peptide nucleic
 18 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 19 and cytosine methylation status in chemically pretreated genomic DNA. The
 20 oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 21 range of diseases including immune system, gastrointestinal, respiratory,
 22 central nervous system, cardiovascular and metabolic disorders. The
 23 oligomers are also used for detecting cell type differentiation.
 24 ABC00010-ABC99989, ABF00010-ABF99989, ASH00010-ASH99989 and
 25 AB100010-AB182073 represent the oligomers described in the invention.
 26 NOTE: The sequence data for this patent did not form part of the printed
 27 specification, but was obtained in electronic format from WIPO at
 28 ftp.wipo.int/pub/published_pct_sequences.
 29 Sequence 13 BP; 7 A; 1 C; 0 G; 4 T; 1 other;
 30 Query Match 1.0%; Score 12.6; DB 1; Length 13;
 31 Best Local Similarity 92.3%; Pred. No. 3.7e+02; Indels 0; Gaps 0;
 32 Matches 12; Conservative 1; Mismatches 0;
 33 1043 APTATTATGTAT 1055
 34 |||||
 35 13 APTATTATGTAT 1
 36
 37 RESULT 658
 38 ABF46540/c
 39 ABF46540 standard; DNA; 13 BP.
 40 ABF46540;
 41 21-FEB-2002 (first entry)
 42 Oligonucleotide SEQ ID NO 146537 for detecting SNP TSC0036949.
 43 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 44 peptide nucleic acid; cytosine methylation; cardiovascular; primer; as;
 45 central nervous system; gastrointestinal; respiratory; immune; metabolic.
 46 Homo sapiens.
 47 WO200177384-A2.
 48 18-OCT-2001.
 49 06-APR-2001; 2001WO-IB00713.
 50 07-APR-2000; 2000DE-1019173.
 51 (EPIG-) EPIGENOMICS AG.
 52 Olek A, Piepenbrock C, Berlin K;
 53 WPI; 2001-657177/75.
 54 Set of oligonucleotides, useful for diagnosis and cell typing, is
 55 designed to detect single nucleotide polymorphisms and cytosine
 56 methylation status -
 57 Claim 1; SEQ ID 146537; 29pp + Sequence Listing; German.
 58 This invention describes novel oligonucleotide primers or peptide nucleic
 59 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 60 and cytosine methylation status in chemically pretreated genomic DNA. The
 61 oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 62 range of diseases including immune system, gastrointestinal, respiratory,
 63 central nervous system, cardiovascular and metabolic disorders. The
 64 oligomers are also used for detecting cell type differentiation.
 65 ABC00010-ABC99989, ABF00010-ABF99989, ASH00010-ASH99989 and
 66 AB100010-AB182073 represent the oligomers described in the invention.
 67 NOTE: The sequence data for this patent did not form part of the printed
 68 specification, but was obtained in electronic format from WIPO at
 69 ftp.wipo.int/pub/published_pct_sequences.
 70 Sequence 13 BP; 7 A; 1 C; 0 G; 4 T; 1 other;
 71 Query Match 1.0%; Score 12.6; DB 1; Length 13;
 72 Best Local Similarity 92.3%; Pred. No. 3.7e+02; Indels 0; Gaps 0;
 73 Matches 12; Conservative 1; Mismatches 0;
 74 1043 APTATTATGTAT 1055
 75 |||||
 76 13 APTATTATGTAT 1
 77
 78 RESULT 658
 79 ABF46540/c
 80 ABF46540 standard; DNA; 13 BP.
 81 ABF46540;
 82 21-FEB-2002 (first entry)
 83 Oligonucleotide SEQ ID NO 146537 for detecting SNP TSC0036949.
 84 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 85 peptide nucleic acid; cytosine methylation; cardiovascular; primer; as;
 86 central nervous system; gastrointestinal; respiratory; immune; metabolic.
 87 Homo sapiens.
 88 WO200177384-A2.
 89 18-OCT-2001.
 90 06-APR-2001; 2001WO-IB00713.
 91 07-APR-2000; 2000DE-1019173.
 92 (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single nucleotide polymorphisms and cytosine
 XX methylation status -
 XX Claim 1; SEQ ID 146537; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation.
 XX ABC00010-ABC99989, ABF00010-ABF99989, ASH00010-ASH99989 and
 XX AB100010-AB182073 represent the oligomers described in the invention.
 XX NOTE: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 6 A; 0 C; 2 G; 4 T; 1 other;
 XX Query Match 1.0%; Score 12.6; DB 1; Length 13;
 XX Best Local Similarity 92.3%; Pred. No. 3.7e+02; Indels 0; Gaps 0;
 XX Matches 12; Conservative 1; Mismatches 0;
 QY 718 AACCTTAATTTCA 730
 Db 13 RACCTTAATTTCA 1
 |||||
 RESULT 659
 ABF46541
 ID ABF46541 standard; DNA; 13 BP.
 AC ABF46541;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 146538 for detecting ng SNP TSC0036949.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; as;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single nucleotide polymorphisms and cytosine
 XX methylation status -
 XX Claim 1; SEQ ID 146538; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

C and cytosine methylation status in chemically pretreated genomic DNA. The
 C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 C range of diseases including immune system, gastrointestinal, respiratory,
 C central nervous system, cardiovascular and metabolic disorders. The
 C oligomers are also used for detecting cell type differentiation.
 C ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 C ABT00010-ABT99989 represent the oligomers described in the invention.
 C NOTE: The sequence data for this patent did not form part of the printed
 C specification, but was obtained in electronic format from WIPO at
 C ftp.wipo.int/pub/published_pct_sequences.

X Sequence 13 BP; 4 A; 2 C; 0 G; 6 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 718 AACTTTAATTCA 730

b 1 RACTTTAATTCA 13

RESULT 660

BF52838
 D ABF52838 standard; DNA; 13 BP.

X ABF52838;

T 21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 152835 for detecting SNP TSC0038627.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 W peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 W central nervous system; gastrointestinal; respiratory; immune; metabolic.

X Homo sapiens.

X WO200177384-A2.

X 18-OCT-2001.

X 06-APR-2001; 2001WO-IB00713.

X 07-APR-2000; 2000DB-1019173.

X (EPIG-) EPIGENOMICS AG.

X Olek A, Piepenbrock C, Berlin K;

X WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -

PS Claim 1; SEQ ID 152835; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic
 C acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 C and cytosine methylation status in chemically pretreated genomic DNA. The
 C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 C range of diseases including immune system, gastrointestinal, respiratory,
 C central nervous system, cardiovascular and metabolic disorders. The
 C oligomers are also used for detecting cell type differentiation.

X ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

X ABT00010-ABT99989 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed
 C specification, but was obtained in electronic format from WIPO at
 C ftp.wipo.int/pub/published_pct_sequences.

X Sequence 13 BP; 4 A; 0 C; 2 G; 6 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1164 AATGATGTTTAT 1176

Db 1 AATGATGTTTAY 13

RESULT 661

ABF52839/C
 ID ABF52839 standard; DNA; 13 BP.

X ABF52839;

X 21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 152836 for detecting SNP TSC0038627.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 W peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 W central nervous system; gastrointestinal; respiratory; immune; metabolic.

X Homo sapiens.

X WO200177384-A2.

X 18-OCT-2001.

X 06-APR-2001; 2001WO-IB00713.

X 07-APR-2000; 2000DB-1019173.

X (EPIG-) EPIGENOMICS AG.

X Olek A, Piepenbrock C, Berlin K;

X WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -

PS Claim 1; SEQ ID 152836; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic
 C acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 C and cytosine methylation status in chemically pretreated genomic DNA. The
 C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 C range of diseases including immune system, gastrointestinal, respiratory,
 C central nervous system, cardiovascular and metabolic disorders. The
 C oligomers are also used for detecting cell type differentiation.

X ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

X ABT00010-ABT99989 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed
 C specification, but was obtained in electronic format from WIPO at
 C ftp.wipo.int/pub/published_pct_sequences.

PS Sequence 13 BP; 6 A; 2 C; 0 G; 4 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1164 AATGATGTTTAT 1176

Db 13 AATGATGTTTAY 1

RESULT 662

ABF53002
 ID ABF53002 standard; DNA; 13 BP.

X

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ABP53002;
21-FEB-2002 (first entry)
Oligonucleotide SEQ ID NO 152999 for detecting SNP TSC0038671.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.
18-OCT-2001.
06-APR-2001; 2001WO-IB00713.
07-APR-2000; 2000DE-1019173.
(EPIG-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single nucleotide polymorphisms and cytosine
methylation status
Claim 1; SEQ ID 152999; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
ABI00010-ABI82073 represent the oligomers described in the invention.
NOTE: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
Sequence 13 BP; 4 A; 0 C; 0 G; 8 T; 1 other;
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
ABI00010-ABI82073 represent the oligomers described in the invention.
NOTE: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
Sequence 13 BP; 4 A; 0 C; 0 G; 8 T; 1 other;
Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1522 TTATATTTTAAAC 1534
|||||
1 TTATATTTTAAAY 13
RESULT 663
BP53003/C
ABP53003 standard; DNA; 13 BP.
ABP53003;
21-FEB-2002 (first entry)
Oligonucleotide SEQ ID NO 153000 for detecting SNP TSC0038671.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.

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XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB00713.
XX 07-APR-2000; 2000DE-1019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status
XX Claim 1; SEQ ID 153000; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABI00010-ABI82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 13 BP; 8 A; 0 C; 0 G; 4 T; 1 other;
XX Query Match 1.0%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.7e+02;
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1522 TTATATTTTAAAC 1534
DB |||||
13 TTATATTTTAAAY 1
RESULT 664
ABP54452
ID ABP54452 standard; DNA; 13 BP.
XX AC ABP54452;
XX 21-FEB-2002 (first entry)
DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 154449 for detecting SNP TSC0039034.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB00713.
XX 07-APR-2000; 2000DE-1019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX

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T Set of oligonucleotides, useful for diagnosis and cell typing, is
 T designed to detect single nucleotide polymorphisms and cytosine
 T methylation status -
 X
 X Claim 1; SEQ ID 154449; 29pp + Sequence Listing; German.
 X
 S This invention describes novel oligonucleotide primers or peptide nucleic
 C acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 C and cytosine methylation status in chemically pretreated genomic DNA. The
 C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 C range of diseases including immune system, gastrointestinal, respiratory,
 C central nervous system, cardiovascular and metabolic disorders. The
 C oligomers are also used for detecting cell type differentiation.
 C ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 C ABH00010-ABH82073 represent the oligomers described in the invention.
 C NOTE: The sequence data for this patent did not form part of the printed
 C specification, but was obtained in electronic format from WIPO at
 C ftp.wipo.int/pub/published_pct_sequences.
 X
 X Sequence 13 BP; 3 A; 0 C; 1 G; 8 T; 1 other;
 X
 Y Query Match 1.0%; Score 12.6; DB 1; Length 13;
 b Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Y 1044 TTATTATGATT 1056
 b 1 TTATTATGATTY 13
 RESULT 665
 BF54453/C
 D ABF54453 standard; DNA; 13 BP.
 X
 X ABF54453;
 X
 X 21-FEB-2002 (first entry)
 X
 X Oligonucleotide SEQ ID NO 154450 for detecting SNP TSC0039034.
 X
 X SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 X peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 X central nervous system; gastrointestinal; respiratory; immune; metabolic.
 X
 X Homo sapiens.
 X
 X WO200177384-A2.
 X
 X 18-OCT-2001.
 X
 X 06-APR-2001; 2001WO-IB00713.
 X
 X 07-APR-2000; 2000DE-1019173.
 X
 X (EPIG-) EPIGENOMICS AG.
 X
 X Olek A, Piepenbrock C, Berlin K;
 X
 X WPI; 2001-657177/75.
 X
 X Set of oligonucleotides, useful for diagnosis and cell typing, is
 X designed to detect single nucleotide polymorphisms and cytosine
 X methylation status -
 X
 X Claim 1; SEQ ID 154450; 29pp + Sequence Listing; German.
 X
 S This invention describes novel oligonucleotide primers or peptide nucleic
 C acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 C and cytosine methylation status in chemically pretreated genomic DNA. The
 C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 C range of diseases including immune system, gastrointestinal, respiratory,
 C central nervous system, cardiovascular and metabolic disorders. The
 C oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABH00010-ABH82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 X Sequence 13 BP; 8 A; 1 C; 0 G; 3 T; 1 other;
 X
 Y Query Match 1.0%; Score 12.6; DB 1; Length 13;
 b Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Y 1044 TTATTATGATT 1056
 b 1 TTATTATGATTY 1
 RESULT 666
 BF57444/C
 D ABF57444 standard; DNA; 13 BP.
 X
 X ABF57444;
 X
 X 21-FEB-2002 (first entry)
 X
 X Oligonucleotide SEQ ID NO 157441 for detecting SNP TSC0007219.
 X
 X SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 X peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 X central nervous system; gastrointestinal; respiratory; immune; metabolic.
 X
 X Homo sapiens.
 X
 X WO200177384-A2.
 X
 X 18-OCT-2001.
 X
 X 06-APR-2001; 2001WO-IB00713.
 X
 X 07-APR-2000; 2000DE-1019173.
 X
 X (EPIG-) EPIGENOMICS AG.
 X
 X Olek A, Piepenbrock C, Berlin K;
 X
 X WPI; 2001-657177/75.
 X
 X Set of oligonucleotides, useful for diagnosis and cell typing, is
 X designed to detect single nucleotide polymorphisms and cytosine
 X methylation status -
 X
 X Claim 1; SEQ ID 157441; 29pp + Sequence Listing; German.
 X
 S This invention describes novel oligonucleotide primers or peptide nucleic
 C acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 C and cytosine methylation status in chemically pretreated genomic DNA. The
 C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 C range of diseases including immune system, gastrointestinal, respiratory,
 C central nervous system, cardiovascular and metabolic disorders. The
 C oligomers are also used for detecting cell type differentiation.
 C ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 C ABH00010-ABH82073 represent the oligomers described in the invention.
 C NOTE: The sequence data for this patent did not form part of the printed
 C specification, but was obtained in electronic format from WIPO at
 C ftp.wipo.int/pub/published_pct_sequences.
 CC
 X Sequence 13 BP; 7 A; 0 C; 0 G; 5 T; 1 other;
 X
 Y Query Match 1.0%; Score 12.6; DB 1; Length 13;
 b Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Y 1482 ATATATATATTTA 1494

13 RTAATATTATTTA 1

SULT 667

IF57445

ABF57445 standard; DNA; 13 BP.

ABF57445;

21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 157442 for detecting SNP TSC0007219.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 157442; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 5 A; 0 C; 0 G; 7 T; 1 other;

Query Match

Best Local Similarity 1.0%; Score 12.6; DB 1; Length 13;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1482 ATATATATTATTTA 1494

1 RTAATATTATTTA 13

SULT 668

F59176

ABF59176 standard; DNA; 13 BP.

ABF59176;

21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 159173 for detecting SNP TSC0040076.

XX

KW

KW

KW

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OS

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PN

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PD

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PP

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PR

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PA

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PI

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DR

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PT

PT

PT

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PS

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CC

CC

CC

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CC

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CC

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status

Claim 1; SEQ ID 159173; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 2 A; 0 C; 1 G; 9 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 3.7e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 986 TTTAAGTTTTTC 998

1 TTTAAGTTTTTT 13

RESULT 669

ABF59177/C

ID ABF59177 standard; DNA; 13 BP.

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AC

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XX

Oligonucleotide SEQ ID NO 159174 for detecting SNP TSC0040076.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

R 07-APR-2000; 2000DE-1019173.
 X (EPIG-) EPIGENOMICS AG.
 A Olek A, Piepenbrock C, Berlin K;
 I WPI; 2001-657177/75.
 X Set of oligonucleotides, useful for diagnosis and cell typing, is
 T designed to detect single nucleotide polymorphisms and cytosine
 T methylation status -
 S Claim 1; SEQ ID 159174; 29pp + Sequence Listing; German.
 X This invention describes novel oligonucleotide primers or peptide nucleic
 C acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 C and cytosine methylation status in chemically pretreated genomic DNA. The
 C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 C range of diseases including immune system, gastrointestinal, respiratory,
 C central nervous system, cardiovascular and metabolic disorders. The
 C oligomers are also used for detecting cell type differentiation.
 C ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 C AB100010-AB182073 represent the oligomers described in the invention.
 C NOTE: The sequence data for this patent did not form part of the printed
 C specification, but was obtained in electronic format from WIPO at
 C ftp.wipo.int/pub/published_pct_sequences.
 X Sequence 13 BP; 9 A; 1 C; 0 G; 2 T; 1 other;
 Q

Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 986 TTTAAGTTTTC 998
 b 13 TTTAAGTTTTC 1

RESULT 670
 ID ABF72046 standard; DNA; 13 BP.
 AC ABF72046;
 X 22-FEB-2002 (first entry)
 X Oligonucleotide SEQ ID NO 172043 for detecting SNP TSC0042899.
 X SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 X peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 X central nervous system; gastrointestinal; respiratory; immune; metabolic.
 X Homo sapiens.
 X WO200177384-A2.
 X 18-OCT-2001.
 X 06-APR-2001; 2001WO-IB00713.
 X 07-APR-2000; 2000DE-1019173.
 X (EPIG-) EPIGENOMICS AG.
 X Olek A, Piepenbrock C, Berlin K;
 X WPI; 2001-657177/75.
 X Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 X Claim 1; SEQ ID 172043; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC AB100010-AB182073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 X Sequence 13 BP; 3 A; 0 C; 2 G; 7 T; 1 other;
 XQ

Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 769 ATCATATAAAAT 781
 Db 13 ATCATATAAAAT 1

RESULT 671
 ABF72047
 ID ABF72047 standard; DNA; 13 BP.
 XX AC ABF72047;
 X 22-FEB-2002 (first entry)
 X Oligonucleotide SEQ ID NO 172044 for detecting SNP TSC0042899.
 X SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 X peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 X central nervous system; gastrointestinal; respiratory; immune; metabolic.
 X Homo sapiens.
 X WO200177384-A2.
 X 18-OCT-2001.
 X 06-APR-2001; 2001WO-IB00713.
 X 07-APR-2000; 2000DE-1019173.
 X (EPIG-) EPIGENOMICS AG.
 X Olek A, Piepenbrock C, Berlin K;
 X WPI; 2001-657177/75.
 X Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 X Claim 1; SEQ ID 172044; 29pp + Sequence Listing; German.
 X This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC AB100010-AB182073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.


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1  Sequence 13 BP; 7 A; 2 C; 0 G; 3 T; 1 other;
Query Match      1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
769 ATCACAATAAAT 781
      |||||
1  ATCACAATAAAT 13
      |||||

SULT 672
F76626
ABF76626 standard; DNA; 13 BP.
ABF76626;
22-FEB-2002 (first entry)
Oligonucleotide SEQ ID NO 176623 for detecting SNP TSC0043824.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.
18-OCT-2001.
06-APR-2001; 2001WO-IB00713.
07-APR-2000; 2000DE-1019173.
(EPIG-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single nucleotide polymorphisms and cytosine
methylation status -
Claim 1; SEQ ID 176623; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
ABI00010-ABI82073 represent the oligomers described in the invention.
NOTE: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
Sequence 13 BP; 3 A; 0 C; 1 G; 8 T; 1 other;
Query Match      1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1045 TATTATGATTT 1057
      |||||
1  TATTATGATTT 13
      |||||

3SULT 673

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ABF76627/c
ID ABF76627 standard; DNA; 13 BP.
XX
AC ABF76627;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 176624 for detecting SNP TSC0043824.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single nucleotide polymorphisms and cytosine
methylation status -
Claim 1; SEQ ID 176624; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
ABI00010-ABI82073 represent the oligomers described in the invention.
NOTE: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
Sequence 13 BP; 8 A; 1 C; 0 G; 3 T; 1 other;
Query Match      1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1045 TATTATGATTT 1057
      |||||
13 TATTATGATTT 1
      |||||

RESULT 674
ABF78844/c
ID ABF78844 standard; DNA; 13 BP.
XX
AC ABF78844;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 178841 for detecting SNP TSC0044293.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

```

S Homo sapiens.
X WO200177384-A2.
X 18-OCT-2001.
X 06-APR-2001; 2001WO-IB00713.
X 07-APR-2000; 2000DE-1019173.
X (EPIG-) EPIGENOMICS AG.
X Olek A, Piepenbrock C, Berlin K;
X WPI; 2001-657177/75.
X Set of oligonucleotides, useful for diagnosis and cell typing, is
T designed to detect single nucleotide polymorphisms and cytosine
T methylation status -
X Claim 1; SEQ ID 178841; 29pp + Sequence Listing; German.
X This invention describes novel oligonucleotide primers or peptide nucleic
X acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
C and cytosine methylation status in chemically pretreated genomic DNA. The
C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
C range of diseases including immune system, gastrointestinal, respiratory,
C central nervous system, cardiovascular and metabolic disorders. The
C oligomers are also used for detecting cell type differentiation.
C ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
C AB100010-AB182073 represent the oligomers described in the invention.
C NOTE: The sequence data for this patent did not form part of the printed
C specification, but was obtained in electronic format from WIPO at
C ftp.wipo.int/pub/published_pct_sequences.
X Sequence 13 BP; 8 A; 0 C; 1 G; 3 T; 1 other;
X This invention describes novel oligonucleotide primers or peptide nucleic
C acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
C and cytosine methylation status in chemically pretreated genomic DNA. The
C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
C range of diseases including immune system, gastrointestinal, respiratory,
C central nervous system, cardiovascular and metabolic disorders. The
C oligomers are also used for detecting cell type differentiation.
C ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
C AB100010-AB182073 represent the oligomers described in the invention.
C NOTE: The sequence data for this patent did not form part of the printed
C specification, but was obtained in electronic format from WIPO at
C ftp.wipo.int/pub/published_pct_sequences.
X Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Y 1560 AAATTTTTTTTAC 1572
b 13 RAATTTTTTTTAC 1
:|||||
RESULT 675
BF78845
ID ABF78845 standard; DNA; 13 BP.
X ABF78845;
X 22-FEB-2002 (first entry)
X Oligonucleotide SEQ ID NO 178842 for detecting SNP TSC0044293.
X SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
X peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
X central nervous system; gastrointestinal; respiratory; immune; metabolic.
X Homo sapiens.
X WO200177384-A2.
X 18-OCT-2001.
X 06-APR-2001; 2001WO-IB00713.
X 07-APR-2000; 2000DE-1019173.
X (EPIG-) EPIGENOMICS AG.
X Olek A, Piepenbrock C, Berlin K;
X WPI; 2001-657177/75.
X Set of oligonucleotides, useful for diagnosis and cell typing, is
T designed to detect single nucleotide polymorphisms and cytosine
T methylation status -
X Claim 1; SEQ ID 178842; 29pp + Sequence Listing; German.
X This invention describes novel oligonucleotide primers or peptide nucleic
X acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
C and cytosine methylation status in chemically pretreated genomic DNA. The
C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
C range of diseases including immune system, gastrointestinal, respiratory,
C central nervous system, cardiovascular and metabolic disorders. The
C oligomers are also used for detecting cell type differentiation.
C ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
C AB100010-AB182073 represent the oligomers described in the invention.
C NOTE: The sequence data for this patent did not form part of the printed
C specification, but was obtained in electronic format from WIPO at
C ftp.wipo.int/pub/published_pct_sequences.
X Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Y 1560 AAATTTTTTTTAC 1572
b 13 RAATTTTTTTTAC 1
:|||||
RESULT 675
BF78845
ID ABF78845 standard; DNA; 13 BP.
X ABF78845;
X 22-FEB-2002 (first entry)
X Oligonucleotide SEQ ID NO 178842 for detecting SNP TSC0044293.
X SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
X peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
X central nervous system; gastrointestinal; respiratory; immune; metabolic.
X Homo sapiens.
X WO200177384-A2.
X 18-OCT-2001.
X 06-APR-2001; 2001WO-IB00713.
X 07-APR-2000; 2000DE-1019173.
X (EPIG-) EPIGENOMICS AG.
X Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX Claim 1; SEQ ID 178842; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC AB100010-AB182073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 13 BP; 3 A; 1 C; 0 G; 8 T; 1 other;
SQ Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1560 AAATTTTTTTTAC 1572
Db 1 RAATTTTTTTTAC 13
:|||||
RESULT 576
ABF79012
ID ABF79012 standard; DNA; 13 BP.
XX ABF79012;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 179009 for detecting SNP TSC0044323.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB00713.
XX 07-APR-2000; 2000DE-1019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX Claim 1; SEQ ID 179009; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 5 A; 0 C; 1 G; 6 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1133 TTATAGTAAATTT 1145

1 TTATAGTAAATTT 13

RESULT 677

ABF79013/c

ABF79013 standard; DNA; 13 BP.

ABF79013;

22-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 179010 for detecting SNP TSC0044323.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status -

Claim 1; SEQ ID 179010; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

AB100010-AB182073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 6 A; 1 C; 0 G; 5 T; 1 other;

Query Match 1.0%; Score 12.6; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 3.7e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1133 TTATAGTAAATTT 1145

DB 13 TTATAGTAAATTT 1

RESULT 678

ABF98558

ID ABF98558 standard; DNA; 13 BP.

XX ABF98558;

AC ABF98558;

XX 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 198555 for detecting SNP TSC0048858.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single nucleotide polymorphisms and cytosine

XX methylation status -

XX Claim 1; SEQ ID 198555; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation.

XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

XX AB100010-AB182073 represent the oligomers described in the invention.

XX NOTE: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 13 BP; 5 A; 0 C; 1 G; 6 T; 1 other;

XX Query Match 1.0%; Score 12.6; DB 1; Length 13;

XX Best Local Similarity 92.3%; Pred. No. 3.7e+02;

XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 523 AAATTGGAATTT 535

DB 1 AAATTGGAATTT 13

RESULT 679

ABF98559/c

ID ABF98559 standard; DNA; 13 BP.

XX ABF98559;

AC ABF98559;

XX

```

TT 22-FEB-2002 (first entry)
TX Oligonucleotide SEQ ID NO 198556 for detecting SNP TSC0048858.
XB
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
X peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
W central nervous system; gastrointestinal; respiratory; immune; metabolic.
W
X Homo sapiens.
X
N WO200177384-A2.
X
D 18-OCT-2001.
F
F 06-APR-2001; 2001WO-IB00713.
X
X 07-APR-2000; 2000DE-1019173.
X (EPiG-) EPIGENOMICS AG.
X Olek A, Piepenbrock C, Berlin K;
X WPI; 2001-657177/75.
X
T Set of oligonucleotides, useful for diagnosis and cell typing, is
T designed to detect single nucleotide polymorphisms and cytosine
T methylation status
T
X Claim 1; SEQ ID 198556; 29pp + Sequence Listing; German.
X
X This invention describes novel oligonucleotide primers or peptide nucleic
X acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
X and cytosine methylation status in chemically pretreated genomic DNA. The
X oligonucleotides are used for diagnosis and/or prognosis of cancer and a
X range of diseases including immune system, gastrointestinal, respiratory,
X central nervous system, cardiovascular and metabolic disorders. The
X oligomers are also used for detecting cell type differentiation.
X ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
X ABH00010-ABH82073 represent the oligomers described in the invention.
X NOTE: The sequence data for this patent did not form part of the printed
X specification, but was obtained in electronic format from WIPO at
X ftp.wipo.int/pub/published_pct_sequences.
X
X Sequence 13 BP; 6 A; 1 C; 0 G; 5 T; 1 other;
X
X This invention describes novel oligonucleotide primers or peptide nucleic
X acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
X and cytosine methylation status in chemically pretreated genomic DNA. The
X oligonucleotides are used for diagnosis and/or prognosis of cancer and a
X range of diseases including immune system, gastrointestinal, respiratory,
X central nervous system, cardiovascular and metabolic disorders. The
X oligomers are also used for detecting cell type differentiation.
X ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
X ABH00010-ABH82073 represent the oligomers described in the invention.
X NOTE: The sequence data for this patent did not form part of the printed
X specification, but was obtained in electronic format from WIPO at
X ftp.wipo.int/pub/published_pct_sequences.
X
X Query Match 1.0%; Score 12.6; DB 1; Length 13;
X Best Local Similarity 92.3%; Pred. NO. 3.7e+02;
X Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Y 523 AAATTGCAATTC 535
b | | | | | | | | | |
X 13 AAATTGCAATTC 1
RESULT 680
ABH23016
ID ABH23016 standard; DNA; 13 BP.
X
X ABH23016;
X
X 22-FEB-2002 (first entry)
X Oligonucleotide SEQ ID NO 222993 for detecting SNP TSC0054291.
X
X SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
X peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
X central nervous system; gastrointestinal; respiratory; immune; metabolic.
X
X Homo sapiens.
X
X WO200177384-A2.
X
X 18-OCT-2001.

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XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX (EPiG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status
XX
XX Claim 1; SEQ ID 222993; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABH00010-ABH82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 3 A; 0 C; 1 G; 8 T; 1 other;
XX
XX Query Match 1.0%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. NO. 3.7e+02;
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1282 ATTATTGTTTATC 1294
Db | | | | | | | | | |
X 1 ATTATTGTTTATC 13
RESULT 681
ABH23017/c
ID ABH23017 standard; DNA; 13 BP.
X
X ABH23017;
X
X 22-FEB-2002 (first entry)
X Oligonucleotide SEQ ID NO 222994 for detecting SNP TSC0054291.
X
X SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
X peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
X central nervous system; gastrointestinal; respiratory; immune; metabolic.
X
X Homo sapiens.
X
X WO200177384-A2.
X
X 18-OCT-2001.
X
X 06-APR-2001; 2001WO-IB00713.
X
X 07-APR-2000; 2000DE-1019173.
X (EPiG-) EPIGENOMICS AG.
X Olek A, Piepenbrock C, Berlin K;
X WPI; 2001-657177/75.
X
X Set of oligonucleotides, useful for diagnosis and cell typing, is
X designed to detect single nucleotide polymorphisms and cytosine
X methylation status

```

T methylation status -
S Claim 1; SEQ ID 222994; 29pp + Sequence Listing; German.
X This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.
ABC00010-ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073 represent the oligomers described in the invention.
NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 8 A; 1 C; 0 G; 3 T; 1 other;
Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1282 ATATTGTTTATC 1294
13 ATATTGTTTATC 1

RESULT 682
ABH36948/C
ABH36948 standard; DNA; 13 BP.
ABH36948;
22-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 236925 for detecting SNP TSC0057806.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.
18-OCT-2001.

06-APR-2001; 2001WO-IB00713.
07-APR-2000; 2000DE-1019173.
(EPIG-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status -
Claim 1; SEQ ID 236925; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.
ABC00010-ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC
CC
XX Sequence 13 BP; 9 A; 0 C; 1 G; 2 T; 1 other;
SQ
Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1561 AATTTTCTTACT 1573
DB 13 RATTTTCTTACT 1

RESULT 683
ABH36949
ID ABH36949 standard; DNA; 13 BP.
XX
AC ABH36949;
XX
DT 22-FEB-2002 (first entry)
XX
DB Oligonucleotide SEQ ID NO 236926 for detecting SNP TSC0057806.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status -
Claim 1; SEQ ID 236926; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.
ABC00010-ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073 represent the oligomers described in the invention.
NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 13 BP; 2 A; 1 C; 0 G; 9 T; 1 other;
Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1561 AATTTTCTTACT 1573
DB 1 RATTTTCTTACT 13

```

RESULT 684
ID ABH40538/c
C ABH40538 standard; DNA; 13 BP.
X
C ABH40538;
X
T 22-FEB-2002 (first entry)
X
E Oligonucleotide SEQ ID NO 240515 for detecting SNP TSC0058679.
X
W SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
W peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
W central nervous system; gastrointestinal; respiratory; immune; metabolic.
X
X Homo sapiens.
X
N WO200177384-A2.
X
D 18-OCT-2001.
X
F 06-APR-2001; 2001WO-IB00713.
X
R 07-APR-2000; 2000DE-1019173.
X
A (EPIG-) EPIGENOMICS AG.
X
I Olek A, Piepenbrock C, Berlin K;
X
R WPI; 2001-657177/75.
X
T Set of oligonucleotides, useful for diagnosis and cell typing, is
T designed to detect single nucleotide polymorphisms and cytosine
T methylation status
X
S Claim 1; SEQ ID 240515; 29pp + Sequence Listing; German.
X
C This invention describes novel oligonucleotide primers or peptide nucleic
C acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
C and cytosine methylation status in chemically pretreated genomic DNA. The
C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
C range of diseases including immune system, gastrointestinal, respiratory,
C central nervous system, cardiovascular and metabolic disorders. The
C oligomers are also used for detecting cell type differentiation.
C ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
C ABT00010-ABT99989 represent the oligomers described in the invention.
C NOTE: The sequence data for this patent did not form part of the printed
C specification, but was obtained in electronic format from WIPO at
C ftp.wipo.int/pub/published_pct_sequences.
X
S Query Match 1.0%; Score 12.6; DB 1; Length 13;
S Best Local Similarity 92.3%; Pred. No. 3.7e+02;
S Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
X
QY 621 AAACACAAATAA 633
DB 13 RAACACAAATAA 1
X
RESULT 685
ABH40539
ID ABH40539 standard; DNA; 13 BP.
X
X ABH40539;
X
T 22-FEB-2002 (first entry)
X
E Oligonucleotide SEQ ID NO 240516 for detecting SNP TSC0058679.
X
W SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
W peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
W central nervous system; gastrointestinal; respiratory; immune; metabolic.
X
X Homo sapiens.
X
N WO200177384-A2.
X
D 18-OCT-2001.
X
F 06-APR-2001; 2001WO-IB00713.
X
R 07-APR-2000; 2000DE-1019173.
X
A (EPIG-) EPIGENOMICS AG.
X
I Olek A, Piepenbrock C, Berlin K;
X
R WPI; 2001-657177/75.
X
T Set of oligonucleotides, useful for diagnosis and cell typing, is
T designed to detect single nucleotide polymorphisms and cytosine
T methylation status
X
S Claim 1; SEQ ID 240515; 29pp + Sequence Listing; German.
X
C This invention describes novel oligonucleotide primers or peptide nucleic
C acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
C and cytosine methylation status in chemically pretreated genomic DNA. The
C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
C range of diseases including immune system, gastrointestinal, respiratory,
C central nervous system, cardiovascular and metabolic disorders. The
C oligomers are also used for detecting cell type differentiation.
C ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
C ABT00010-ABT99989 represent the oligomers described in the invention.
C NOTE: The sequence data for this patent did not form part of the printed
C specification, but was obtained in electronic format from WIPO at
C ftp.wipo.int/pub/published_pct_sequences.
X
S Query Match 1.0%; Score 12.6; DB 1; Length 13;
S Best Local Similarity 92.3%; Pred. No. 3.7e+02;
S Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
X
QY 621 AAACACAAATAA 633
DB 13 RAACACAAATAA 1
X

```

```

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PP WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
DR designed to detect single nucleotide polymorphisms and cytosine
DR methylation status
XX
PS Claim 1; SEQ ID 240516; 29pp + Sequence Listing; German.
XX
C This invention describes novel oligonucleotide primers or peptide nucleic
C acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
C and cytosine methylation status in chemically pretreated genomic DNA. The
C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
C range of diseases including immune system, gastrointestinal, respiratory,
C central nervous system, cardiovascular and metabolic disorders. The
C oligomers are also used for detecting cell type differentiation.
C ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
C ABT00010-ABT99989 represent the oligomers described in the invention.
C NOTE: The sequence data for this patent did not form part of the printed
C specification, but was obtained in electronic format from WIPO at
C ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Query Match 1.0%; Score 12.6; DB 1; Length 13;
SQ Best Local Similarity 92.3%; Pred. No. 3.7e+02;
SQ Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
X
QY 621 AAACACAAATAA 633
DB 13 RAACACAAATAA 13
X
RESULT 686
ABH50358
ID ABH50358 standard; DNA; 13 BP.
XX
XX ABH50358;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 250335 for detecting SNP TSC0061125.
XX
X SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
X peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
X central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX

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(EPIG-) EPIGENOMICS AG.
 Olek A, Piepenbrock C, Berlin K;
 WPI; 2001-657177/75.
 Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status
 Claim 1; SEQ ID 250335; 29pp + Sequence Listing; German.
 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.
 ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT99989 represent the oligomers described in the invention.
 NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 Sequence 13 BP; 2 A; 0 C; 2 G; 8 T; 1 other;
 Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1455 TTGTTTATTATGT 1467
 |||||
 1 TTGTTTATTATGY 13
 RESULT 687
 HS0359/c
 ABH50359 standard; DNA; 13 BP.
 ABH50359;
 22-FEB-2002 (first entry)
 Oligonucleotide SEQ ID NO 250336 for detecting SNP TSC061125.
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
 Homo sapiens.
 WO200177384-A2.
 18-OCT-2001.
 06-APR-2001; 2001WO-IB00713.
 07-APR-2000; 2000DE-1019173.
 (EPIG-) EPIGENOMICS AG.
 Olek A, Piepenbrock C, Berlin K;
 WPI; 2001-657177/75.
 Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status
 Claim 1; SEQ ID 250336; 29pp + Sequence Listing; German.
 This invention describes novel oligonucleotide primers or peptide nucleic

acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.
 ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT99989 represent the oligomers described in the invention.
 NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 Sequence 13 BP; 8 A; 2 C; 0 G; 2 T; 1 other;
 Query Match 1.0%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1455 TTGTTTATTATGT 1467
 |||||
 13 TTGTTTATTATGY 1
 RESULT 688
 ABH58638
 ID ABH58638 standard; DNA; 13 BP.
 AC ABH58638;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX Oligonucleotide SEQ ID NO 258615 for detecting SNP TSC0062878.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
 KW
 KW Homo sapiens.
 XX
 OS WO200177384-A2.
 XX
 PN 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB00713.
 PF
 XX 07-APR-2000; 2000DE-1019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status
 PT
 PT Claim 1; SEQ ID 258615; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.
 CC
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT99989 represent the oligomers described in the invention.
 CC
 CC NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC
 CC Sequence 13 BP; 3 A; 0 C; 2 G; 7 T; 1 other;
 XX

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Query Match          1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 545 TGAATAGTTTTC 557
b 1 TGAATAGTTTTC 13

RESULT 689
BH58639/C
D ABH58639 standard; DNA; 13 BP.
X
X ABH58639;
X
X 22-FEB-2002 (first entry)
X
X Oligonucleotide SEQ ID NO 258616 for detecting SNP TSC0062878.
X
X SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
X peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
X central nervous system; gastrointestinal; respiratory; immune; metabolic.
X
X Homo sapiens.
X
X WO200177384-A2.
X
X 18-OCT-2001.
X
X 06-APR-2001; 2001WO-IB00713.
X
X 07-APR-2000; 2000DE-1019173.
X
X (EPIG-) EPIGENOMICS AG.
X
X Olek A, Piepenbrock C, Berlin K;
X
X WPI; 2001-657177/75.
X
X Set of oligonucleotides, useful for diagnosis and cell typing, is
X designed to detect single nucleotide polymorphisms and cytosine
X methylation status -
X
X Claim 1; SEQ ID 258616; 29pp + Sequence Listing; German.
X
X This invention describes novel oligonucleotide primers or peptide nucleic
X acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
X and cytosine methylation status in chemically pretreated genomic DNA. The
X oligonucleotides are used for diagnosis and/or prognosis of cancer and a
X range of diseases including immune system, gastrointestinal, respiratory,
X central nervous system, cardiovascular and metabolic disorders. The
X oligomers are also used for detecting cell type differentiation.
X
X AB000010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
X AB100010-AB182073 represent the oligomers described in the invention.
X NOTE: The sequence data for this patent did not form part of the printed
X specification, but was obtained in electronic format from WIPO at
X ftp.wipo.int/pub/published_pct_sequences.
X
X Sequence 13 BP; 7 A; 2 C; 0 G; 3 T; 1 other;

Query Match          1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Y 545 TGAATAGTTTTC 557
b 13 TGAATAGTTTTC 1

RESULT 690
BH60060
D ABH60060 standard; DNA; 13 BP.

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XX ABH60060;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 260037 for detecting SNP TSC0007828.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB00713.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX
XX Claim 1; SEQ ID 260037; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX
XX AB000010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX AB100010-AB182073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 4 A; 0 C; 1 G; 7 T; 1 other;

Query Match          1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1428 TATTAGTAATTC 1440
Db 1 TATTAGTAATTC 13

RESULT 691
ABH60061/C
ID ABH60061 standard; DNA; 13 BP.
XX
XX ABH60061;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 260038 for detecting SNP TSC0007828.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX

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oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and
CC ABT00010-ABT82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
X ftp.wipo.int/pub/published_pct_sequences.
Q Sequence 13 BP; 5 A; 0 C; 0 G; 7 T; 1 other;
Query Match 1.0%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Y 1616 TAAATATATATTT 1628
b 13 TAAATATATATTT 1
RESULT 694
AD49641
D AAD49641 standard; mRNA; 15 BP.
X C
X C AAD49641;
X T
X 24-MAR-2003 (first entry)
X Human adenylate uridylylate-rich element (ARE) motif mRNA #3.
X MyoDosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer;
X gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis;
X autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic;
X neurodegenerative disorder; Parkinson's disease; gene therapy; virucide;
X haemostatic; antibacterial; nootropic; neuroprotective; cytostatic;
X fungicide; human; adenylate uridylylate-rich element; ARE; ss.
X Homo sapiens.
X WO200283953-A1.
X 24-OCT-2002.
X 11-APR-2002; 2002WO-US11757.
X 11-APR-2001; 2001US-282965P.
X (PTCT-) PTC THERAPEUTICS INC.
X Rando R, Welch E;
X WPI; 2003-075561/07.
X Identifying a test compound that binds to a target RNA molecule for
X treating or preventing amyloidosis, hemophilia, cancer, gigantism,
X diabetes, by contacting a detectably labeled target RNA molecule with a
X library of test compounds -
X Disclosure; Page 18; 152pp; English.
X The invention relates to a method for identifying a test compound that
X binds to a target RNA molecule, which comprises contacting a detectably
X labelled target RNA molecule with a library of test compounds under
X conditions that permit direct binding of the labelled target RNA to a
X member of the library of test compounds so that a detectably labeled
X target RNA: test compound complex is formed. The method is useful for
X screening libraries of compounds for those that are selectively bind to
X a pre-selected target RNA. The compounds are useful for inhibiting the
X formation of a specific bound RNA: host cell factor complexes in vivo.
X They are also useful for treating or preventing diseases associated
X with overproduction or decreased protein function, such as amyloidosis,
X haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism,
X dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging,
X inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative
X disorders, Parkinson's disease or infections (bacterial, viral, fungal).

The invention is also used in gene therapy. The present sequence is
CC human adenylate uridylylate-rich element (ARE) motif mRNA. This sequence
CC is used to illustrate the method of the invention.
X X
SQ Sequence 15 BP; 4 A; 0 C; 0 G; 9 U; 2 other;
Query Match 1.0%; Score 12.6; DB 1; Length 15;
Best Local Similarity 26.7%; Pred. No. 4.2e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
QY 1045 TATTATGCTATTAT 1059
Db 1 WATUUUUUUUUUAW 15
RESULT 695
AAL50230
ID AAL50230 standard; mRNA; 15 BP.
X X
X AC AAL50230;
X X
X DT 13-FEB-2003 (first entry)
X X
X DE Human ARE-mRNA sequence #3.
X X
X KW ARE-mRNA; protein secretion inhibition; ARE-mRNA regulation;
X inflammation; arthritis; autoimmune disease; septic shock; blood clot;
X stroke; INFAlpha; tumour necrosis factor alpha; antiinflammatory;
X antiarthritic; antibacterial; immunosuppressive; cerebroprotective;
X antipruritic; immunomodulator; adenylate-uridylylate rich element; ss.
X Homo sapiens.
X WO200283842-A2.
X X
X PD 24-OCT-2002.
X X
X PF 08-APR-2002; 2002WO-US10898.
X X
X PR 10-APR-2001; 2001US-282974P.
X X
X PA (MESS-) MESSAGE PHARM INC.
X X
X PI Giordano T, Sturgess MA;
X X
X WPI; 2003-046924/04.
X Modulating Adenylate-Uridylate Rich element-mRNA regulation involves
X administering new amide compound that inhibits secretion of protein
X encoded by ARE-mRNA, useful for treating inflammation, arthritis and
X autoimmune diseases -
X Disclosure; Fig 5; 147pp; English.
X The present invention relates to a method of modulating the regulation of
X an adenylate-uridylylate rich element (ARE)-mRNA, which involves
X administering new compounds that inhibits secretion of a protein encoded
X by an ARE-mRNA. This can be used in the treatment of inflammation, fever,
X arthritis, autoimmune diseases, septic shock, blood clot, stroke, fever,
X acute respiratory distress syndrome (ARDS) and cachexia. The present
X sequence is an ARE-mRNA shown in the exemplification of the invention.
X X
SQ Sequence 15 BP; 4 A; 0 C; 0 G; 1 T; 8 U; 2 other;
Query Match 1.0%; Score 12.6; DB 1; Length 15;
Best Local Similarity 33.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
QY 1045 TATTATGCTATTAT 1059
Db 1 WATUUUUUUUUUAW 15

OS	Humicola grisea.
XX	EP215594-A.
XX	25-MAR-1987.
XX	27-AUG-1986; 86EP-0306624.
XX	29-AUG-1985; 85US-0771374.
PR	29-AUG-1985; 85US-0771394.
XX	07-JUL-1986; 86US-0862224.
XX	(GENV) GENENCOR INC.
XX	Cullen D, Gray GL, Hayenga KJ, Lawlis VB;
DR	WPI; 1987-095049/14.
XX	New DNA sequences for expressing polypeptide in filamentous fungi
PPT	- with secretion of prod. from the cells, and new vectors and
PT	transformed fungi
XX	Example; Fig 20; 45pp; English.
PS	A DNA sequence coding for a heterologous polypeptide which can be
XX	expressed in and secreted from filamentous fungi is claimed. Pref.
CC	the DNA sequence codes for bovine preprochymosin, M. mehei
CC	preprocarboxyl protease or A. niger preglucoamylase. Also new
CC	are vectors consisting of the DNA sequence plus an operably-linked
CC	signal sequence. The vectors may also include a sequence which
CC	increases transformation efficiency, e.g. AMS-1.
CC	(Updated on 25-MAR-2003 to correct PR field.)
CC	(Updated on 25-MAR-2003 to correct PA field.)
XX	Sequence 17 BP; 8 A; 1 C; 0 G; 3 T; 5 other;
SQ	
Query Match	1.0%; Score 12.6; DB 1; Length 17;
Best Local Similarity	66.7%; Pred. NO. 4.7e+02;
Matches	10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY	1271 AGTATAGTAGTCATTATA 1285 ::: ::: ::: ::: 2 ARTAYARTAYATHA 16
DB	
RESULT 698	
AAQ078885	
ID	AAQ078885 standard; DNA; 17 BP.
XX	AC AAQ078885;
XX	25-MAR-2003 (updated)
DT	18-DEC-1995 (first entry)
DT	
DE	Humicola grisea glucoamylase hybridization probe.
XX	
KW	Glucoamylase; DNA probe; gene cloning; protein secretion; ss.
XX	Synthetic.
OS	EP625577-A1.
XX	23-NOV-1994.
XX	27-AUG-1986; 94EP-0201751.
PP	
XX	29-AUG-1985; 85US-0771374.
PR	07-JUL-1986; 86US-0862224.
PR	27-AUG-1986; 86EP-0306624.
XX	(GENV) GENENCOR INT INC.
PA	
XX	Berka RM, Cullen D, Gray GL, Hayenga KJ, Lawlis VB;

XX WPI; 1994-359750/45.
 CC Vectors and DNA for expressing polypeptide(s) in filamentous fungi
 CC - include secretory signal sequences that are native or foreign to
 CC heterologous polypeptide(s), such as chymosin or glucoamylase.
 XX Example 9A3; Page 22; 50pp; English.
 CC The DNA probe and corresponding probes covering the degenerate
 CC sites (AAQ78886-Q78891) correspond to amino acids 17-22 of the
 CC H. grisea glucoamylase peptide GAI (AAK62933), and are used as
 CC hybridization probes to detect and isolate H. grisea glucoamylase
 CC DNA in a Southern blot. Resulting genomic DNA fragments are
 CC excised and cloned in plasmid pKSH1. This illustrates the main
 CC claims of the patent, i.e. a vector containing (i) DNA encoding
 CC a heterologous polypeptide (chymosin, prochymosin, preprochymosin,
 CC Aspergillus niger glucoamylase, H. grisea glucoamylase, or Mucor
 CC miehei carboxyl protease) and (ii) a secretory signal peptide,
 CC and a filamentous fungus (Aspergillus or Trichoderma, Neurospora,
 CC Podospora, Endothia, Mucor, Cochicobolus or Pyricularia, especially
 CC A. nidulans, A. awamori or T. reesei) transformed with the vector
 CC for recombinant protein (enzyme) production.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX Sequence 17 BP; 8 A; 1 C; 0 G; 3 T; 5 other;
 Query Match 1.0%; Score 12.6; DB 1; Length 17;
 Best Local Similarity 66.7%; Pred. No. 4.7e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1271 AGTATAGTACATTA 1285
 b :|||:|||:|:
 2 ARTAYARTAYATTA 16
 RESULT 699
 BK85464/C
 D ABK85464 standard; cDNA; 18 BP.
 C ABK85464;
 X 16-AUG-2002 (first entry)
 X 5'-degenerate sequence of shrimp alkaline phosphatase (SAP) cDNA.
 X Shrimp; heat labile alkaline phosphatase; SAP; DNA sequencing reaction;
 X cloning vector dephosphorylation; PCR amplification product-mixture;
 X reporter enzyme; gene; ss.
 X Pandanus borealis.
 X WO200231157-A2.
 X 18-APR-2002.
 X 10-OCT-2001; 2001WO-GB04503.
 X 10-OCT-2000; 2000GB-0024827.
 X (NOFI-) NORWEGIAN INST FISHERIES & AQUACULTURE.
 X (GARD/) GARDNER R.
 X Gardner R, Nilsen I, Oeverboe K;
 X WPI; 2002-444182/47.
 X Novel recombinant heat labile shrimp alkaline phosphatase useful in
 X molecular biology techniques, in the production of DNA based
 X therapeutics or in forensic science, and for laboratory protocols -
 X Disclosure; Page 15; 54pp; English.

XX The present invention relates to the isolation of shrimp (Pandalus
 CC borealis) heat labile alkaline phosphatase (S.C. 3.1.3.1) referred
 CC to as SAP, and polynucleotide sequences encoding it. The SAP enzyme
 CC is useful in the dephosphorylation of cloning vectors prior to
 CC ligation reactions, in the treatment of PCR amplification
 CC product-mixtures prior to DNA sequencing reactions, in molecular
 CC biology techniques, in the production of DNA based therapeutics or
 CC in forensic science, for laboratory protocols, and as a reporter
 CC enzyme. The SAP enzyme is heat labile and cold active making it
 CC particularly suitable for use in multi-step laboratory protocols
 CC where a simple heating step deactivates the enzyme. The present
 CC sequence represents the missing 5'-sequence of the cDNA encoding
 CC SAP.
 XX Sequence 18 BP; 7 A; 1 C; 3 G; 2 T; 5 other;
 Query Match 1.0%; Score 12.6; DB 1; Length 18;
 Best Local Similarity 66.7%; Pred. No. 4.9e+02;
 Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 886 CTGTGTCCTACTGTCCTT 903
 Db :|||:|||:|:
 18 YTRTTCCTANGCYTT 1
 RESULT 700
 AAV22349/C
 ID AAV22349 standard; RNA; 14 BP.
 XX AC AAV22349;
 XX 29-JUN-1998 (first entry)
 XX A promoter regulatory motif found in the utrons of the invention.
 DE 3' untranslated region; UTR; inhibition; gene expression; ICM-7;
 XX interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;
 KW antigen expression; gene promoter; utron; B7-1; B7-2; Fc gamma R;
 KW HIV gene expression; transplant rejection; treatment;
 KW autoimmune disease; inflammatory disease; ss.
 XX Unidentified.
 OS WO9744450-A1.
 XX 27-NOV-1997.
 XX 21-MAY-1997; 97WO-US09459.
 XX 21-MAY-1996; 96US-0646789.
 XX (UYTA) UNIV YALE.
 XX Peyman JA;
 XX WPI; 1998-018505/02.
 XX Utrons, RNA molecules containing promoter regulatory motifs -
 PT useful to suppress expression from promoter of interest,
 PT specifically TSU nucleic acid suppression of MHC Class I and II gene
 PT expression
 XX Claim 20; Page 20; 200pp; English.
 XX The present sequence represents a promoter regulatory element,
 CC found in the utrons of the invention. Utrons are from, or are
 CC homologous to, the 3' untranslated region (UTR), of an mRNA that
 CC stimulates or inhibits a cellular response by sequence specific
 CC interactions. The utron is able to suppress constitutive and
 CC interferon-gamma (IFN-gamma) induced major histocompatibility complex
 CC (MHC) class I and class II antigen expression and expression of other
 CC antigens, the gene promoters of which contain related sequence motifs

that are stimulated by the same factors which stimulate MHC class I and class II antigen expression. Such utrons can be used to regulate gene expression in a subject, e.g. a human or a cell in vitro, specifically inhibiting MHC class I or II. ICAM-7, B7-1, B7-2, FC gamma R, IL-2 or HIV gene expression. They can be used to inhibit transplant rejection, or treat an autoimmune or inflammatory disease or disorder.

Sequence 14 BP; 5 A; 2 C; 2 G; 5 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 4.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1016 TTTCAGTGTAACT 1029

|||||
14 TTTCAGTGTAACT 1

RESULT 701

AV22279/C

AAV22279 standard; DNA; 14 BP.

AAV22279;

29-JUN-1998 (first entry)

ISRE gene promoter motif found in a trophoblast STAT utron.

Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition; interferon-gamma; IFN-gamma; major histocompatibility complex; MHC; antigen expression; gene promoter; class I; class II; IFN signalling; GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7; B7-1; B7-2; FC gamma R; HIV gene expression; transplant rejection; treatment; autoimmune disease; inflammatory disease; SS.

Unidentified.

WO9744450-A1.

27-NOV-1997.

21-MAY-1997; 97WO-US09459.

21-MAY-1996; 96US-0646789.

(UTYA) UNIV YALE.

Peyman JA;

WPI; 1998-018505/02.

Utrons, RNA molecules containing promoter regulatory motifs - useful to suppress express expression from promoter of interest, specifically TSU nucleic acid suppression of MHC Class I and II gene expression

Disclosure; Page 90; 200pp; English.

The present sequence represents an ISRE gene promoter motif found in a trophoblast STAT utron (TSU). TSUs be isolated from a CDNA library prepared from mRNA isolated from trophoblast cells. Utrons are from, or are homologous to, the 3' untranslated region (UTR), of an mRNA that stimulates or inhibits a cellular response by sequence specific interactions. The TSU is able to suppress constitutive and interferon-gamma (IFN-gamma) induced major histocompatibility complex (MHC) class I and class II antigen expression and expression of other antigens, the gene promoters of which contain related sequence motifs that are stimulated by the same factors which stimulate MHC class I and class II antigen expression. The TSU sequence contains motifs related to IFN signalling (GAS, ISRE and interleukin-4 response elements). The nucleic acid can be used to regulate gene expression in a subject, e.g. a human or a cell in vitro, specifically inhibiting MHC Class I or II,

ICAM-7, B7-1, B7-2, FC gamma R, IL-2 or HIV gene expression. It can be used to inhibit transplant rejection, or treat an autoimmune or inflammatory disease or disorder. It can also be used to inhibit the action of SPAT-6, or a cytokine.

Sequence 14 BP; 5 A; 2 C; 2 G; 5 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 4.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1016 TTTCAGTGTAACT 1029

Db 14 TTTCAGTGTAACT 1

RESULT 702

AAZ32432

ID AAZ32432 standard; DNA; 14 BP.

AC AAZ32432;

DT 26-JAN-2000 (first entry)

8-mer minor groove binder conjugated oligonucleotide SEQ ID NO:37.

M13mp19; MGB; minor groove binder; hybridisation; conjugate; mismatch discrimination; diagnosis; detection; primer; probe; forensic analysis; SS.

Synthetic.

WO9951621-A2.

14-OCT-1999.

05-APR-1999; 99WO-US07487.

03-APR-1998; 98US-0054832.

(BPOC-) EPOCH PHARM INC.

Hedgpeth J, Afonina IA, Kutyavin IV, Lukhtanov EA, Belousov BS; Meyer RB;

WPI; 1999-633727/54.

Hybridization process using oligonucleotide primer or probe that is conjugated to minor groove binder, e.g. for amplification reactions or assays for mutations

Example 6; Page 68; 95pp; English.

A method has been developed for hybridising two nucleic acids (NA) in which at least one NA comprises a minor groove binder (MGB) - oligonucleotide conjugate (A). MGB is a molecule of 150-2000 D that binds in a non-intercalating manner to the minor groove of a double-stranded NA. Hybridisation with (A), particularly where this is a probe or primer, is used: in primer extension (amplification) reactions; to identify single-nucleotide (nt) mismatches; in ligation reactions; in sequencing; for analysis of gene expression and detection of mutations; for detecting target nucleic acids (especially for diagnosis or forensic analysis, e.g. to detect human immune deficiency virus or to differentiate between its subtypes, including those that are resistant to antiviral agents) and for cDNA synthesis. (A) forms hybrids with complementary target sequences of very high stability, so even short probes, e.g. 8-mers, are highly specific and efficient. (A) also improve the discriminatory capacity of short oligonucleotides, providing better detection of single-base mismatches, and the speed (more rapid annealing to target) and versatility of assays are increased. Short primers are easier, and less expensive, to produce. The present sequence represents an 8-mer minor groove binder conjugated oligonucleotide used in an example from the present invention.

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CX IQ Sequence 14 BP; 1 A; 1 C; 2 G; 10 T; 0 other;
    Query Match 1.0%; Score 12.4; DB 1; Length 14;
    Best Local Similarity 92.9%; Pred. No. 4.3e+02;
    Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

NY 1564 TTTTCTTACTGTTT 1577
    ||||| |||||
    1 TTTTGTTTACTGTTT 14

RESULT 703
RAD20794
D AAD20794 standard; DNA; 14 BP.
X C AAD20794;
X X 04-JAN-2002 (first entry)
X X FNA16/DNA oligo, used in sequencing and mass spectrometer detection.
X X Mass spectrometry; diagnosis; genetic disease; chromosomal abnormality;
X X obesity; atherosclerosis; cancer; infection; viral; bacterial; fungal;
X X matrix-assisted laser desorption/ionisation; MALDI; HLA phenotyping;
X X heredity; mass spectrometry; ss.
X X Unidentified.
X X US6300076-B1.
X X 09-OCT-2001.
X X 31-JAN-2000; 2000US-0495444.
X X 18-MAR-1996; 96US-0617256.
X X 17-MAR-1995; 95US-0406199.
X X (SEQU-) SEQUENOM INC.
X X Koester H;
X X WPI; 2001-624663/72.
X X Detecting target nucleic acid sequences in a biological sample
X X comprises amplifying NA molecules and analyzing using matrix-assisted
X X laser desorption/ionization time of flight mass spectrometry -
X X Example 9; Column 35; 90pp; English.
X X The invention relates to mass spectrometric processes useful for
X X detecting nucleic acids in a biological sample, comprises amplifying
X X nucleic acid molecules and analyzing using matrix-assisted laser
X X desorption/ionisation (MALDI) time-of-flight (TOF) mass spectrometry.
X X The methods are used to diagnose (e.g., prenatally or postnatally) a
X X genetic disease or chromosomal abnormality; a predisposition to a disease
X X or condition (e.g., obesity, atherosclerosis, cancer), or infection by a
X X pathogenic organism (e.g., virus, bacteria, parasite or fungus); or to
X X provide information relating to identity, heredity, or compatibility
X X (e.g., HLA phenotyping). The present sequence is oligonucleotide,
X X FNA16/DNA used in solid state sequencing and mass spectrometer detection.
X X Sequence 14 BP; 4 A; 4 C; 2 G; 4 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DY 458 TCACACTTCATGT 471
    ||||| |||||
    1 TCACACTTCATGT 14

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RESULT 704
AAS10742
ID AAS10742 standard; DNA; 14 BP.
XX AC AAS10742;
XX XX 24-OCT-2001 (first entry)
XX XX Solid-state DNA sequencing primer FNA16/DNA.
XX XX mass spectrometry; DNA fingerprint; obesity; atherosclerosis;
XX KW cancer; chromosomal abnormality; fungal; bacterial; protist; infection;
XX KW human leukocyte antigen; HLA genotyping; apolipoprotein E gene;
XX KW variable number of tandem repeat; VNTR; nucleic acid detection;
XX XX ss; sequencing primer.
XX XX Synthetic.
XX XX US6258538-B1.
XX XX 10-JUL-2001.
XX XX 06-APR-1999; 99US-0287679.
XX XX 18-MAR-1996; 96US-0617256.
XX PR 06-APR-1999; 99US-0287679.
XX PR 17-MAR-1995; 95US-0406199.
XX XX (SEQU-) SEQUENOM INC.
XX XX Koester H, Little DP, Braun A;
XX XX WPI; 2001-450360/48.
XX XX Use of mass spectrometry for identifying or detecting target
XX XX nucleotide(s) present in nucleic acid molecule(s) -
XX XX Example 9; Column 35; 95pp; English.
XX XX The sequence represents solid-state DNA sequencing primer FNA16/DNA
XX XX used to demonstrate the method of the invention. This involves use of
XX XX mass spectrometry for identifying target nucleotide(s) present in nucleic
XX XX acid molecule(s), detecting a target nucleotide present in a biological
XX XX sample and determining whether a target nucleotide is present in nucleic
XX XX acid molecule(s). The method is used for identifying target nucleotide(s)
XX XX present in a DNA or RNA molecule(s), detecting a target nucleotide
XX XX present in a biological sample and determining whether a target
XX XX nucleotide present in nucleic acid molecule(s). The target nucleotides
XX XX are identified and detected in nucleic acid molecule(s) obtained from an
XX XX individual, and the target nucleotide(s) provides a DNA fingerprint or is
XX XX indicative of a genetic disease (such as obesity, atherosclerosis,
XX XX cancer), chromosomal abnormality (either prenatally or postnatally), a
XX XX genetic predisposition, a fungal, bacterial, or protist infection. The
XX XX presence of the target nucleotide also indicates the presence of a
XX XX mutation. They also provide information relating to identity, heredity,
XX XX or compatibility (human leukocyte antigen (HLA) genotyping). The method
XX XX is suitable for the detection of single point mutations or microlesions
XX XX of DNA and is also applicable in each disease gene or polymorphic region
XX XX in the genome e.g. variable number of tandem repeats (VNTR) or other
XX XX single nucleotide polymorphisms (e.g. apolipoprotein E gene). The
XX XX processes described above provide for increased accuracy and reliability
XX XX of nucleic acid detection by mass spectrometry, in addition the processes
XX XX allow for regress controls to prevent false positive or false negative
XX XX results.
XX XX Sequence 14 BP; 4 A; 4 C; 2 G; 4 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 458 TCACACTTCATGT 471
    ||||| |||||

```

1 TCAACACTGCATGT 14

SULT 705
D07293

AAD07293 standard; cDNA; 14 BP.

AAD07293;

06-AUG-2001 (first entry)

PNA16/DNA primer.

Diagnosis; genetic disease; chromosomal abnormality; infection;
heredity; mass spectrometry; primer; ss.

Unidentified.

US6221601-B1.

24-APR-2001.

02-NOV-1999; 99US-0431613.

18-MAR-1996; 96US-0617256.

17-MAR-1995; 95US-0406199.

(SEQU-) SEQUENOM INC.

Koester H, Higgins GS, Little DP, Braun A;

WPI; 2001-327240/34.

Detecting a target nucleic acid sequence, useful for diagnosing a
genetic disease, a chromosomal abnormality or an infection by a
pathogen, or for determining identity or heredity, by employing mass
spectrometry-based processes -

Example 9; Column 35; 94pp; English.

The present invention relates to detecting a target nucleic acid
sequence, useful for diagnosing a genetic disease, a chromosomal
abnormality or an infection by a pathogen and for determining identity
or heredity by employing mass spectrometry-based processes. The method
involves hybridising a primer to a nucleic acid molecule comprising a
target nucleic acid sequence, extending the primer using a polymerase
to produce an extension product, selectively cleaving the 5' end of the
primer from the extension product, to produce a portion of the primer and
a cleaved extension product and detecting the cleaved extension product
by mass spectrometry. The present sequence is a primer used in solid
state sequencing and mass spectrometer detection.

Sequence 14 BP; 4 A; 4 C; 2 G; 4 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred No. 4.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 458 TCAACACTGCATGT 471

|||||
1 TCAACACTGCATGT 14

RESULT 706

BK98758

D ABK98758 standard; DNA; 14 BP.

C ABK98758;

21-OCT-2002 (first entry)

Solid state sequencing reaction product #1.

DNA diagnostic mass spectrometry; ds; genetic disease;
chromosomal abnormality; viral infection; fungal infection;
bacterial infection; protist infection; human leukocyte antigen;
HLA phenotyping.

Synthetic.

US6277573-B1.

21-AUG-2001.

06-APR-1999; 99US-0287681.

18-MAR-1996; 96US-0617256.

17-MAR-1995; 95US-0406199.

(SEQU-) SEQUENOM INC.

Koester H;

WPI; 2001-540404/60.

Detecting target nucleic acid sequence in sample, useful for diagnosing
genetic disease or chromosomal abnormality, comprises amplifying
nucleic acid containing target sequence and detecting amplified product
by mass spectrometry -

Example 9; Column 38; 92pp; English.

The invention relates to a method of detecting target nucleic acid
sequences (S) in a biological sample, comprising performing on nucleic
acid molecule(s) containing (S), a first polymerase chain reaction (PCR)
to produce a first amplification product (P1), performing on P1 a second
PCR to produce a second amplification product (P2), and detecting P2 by
mass spectrometry, thus detecting the presence of (S) in the biological
sample. The method is useful for detecting the presence of target nucleic
acid sequence(s) in a biological sample obtained from an individual, and
detecting (S) provides a DNA fingerprint or is indicative of a disease or
condition such as genetic disease, chromosomal abnormality, genetic
predisposition, viral infection, fungal infection, bacterial infection,
and protist infection. The method is useful to diagnose (e.g., prenatally
or postnatally) a genetic disease or chromosomal abnormality, a
predisposition to a disease or condition (e.g., obesity, atherosclerosis,
cancer), or infection by a pathogenic organism (e.g. virus, bacteria,
parasitic or fungus), or to provide information relating to identity
heredity, or compatibility (e.g. human leukocyte antigen (HLA)
phenotyping). The method is fast, highly accurate and reliable.
ABK98702-ABK98839 represent primers and DNA sequences used in examples
which demonstrate the method of the invention.

Sequence 14 BP; 4 A; 4 C; 2 G; 4 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred No. 4.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 458 TCAACACTGCATGT 471

|||||
1 TCAACACTGCATGT 14

RESULT 707

ABL55256/c

ID ABL55256 standard; DNA; 14 BP.

XX ABL55256;

AC ABL55256;

XX 28-JUN-2002 (first entry)

Vector 1-8 Sleeping Beauty transposon 3' flanking sequence.
Transgenic mammal; transposon; non-integrated; signature site;
transposase; disease model; drug screening; xenotransplant;

GW Sleeping Beauty; flanking sequence; vector; ds.
 XX Synthetic.
 XX WO200213602-A1.
 XX 21-FEB-2002.
 XX 08-JUN-2001; 2001WO-JP04862.
 XX 16-AUG-2000; 2000JP-0247060.
 XX (KANS-) KANSAI TECHNOLOGY LICENSING ORG CO LTD.
 XX (TAKE/) TAKEDA J.
 XX Takeda J, Horie K;
 XX WPI; 2002-241819/29.
 XX Transgenic non-human mammals containing non-integrated transposon
 XX and/or transposase gene, useful as disease models for e.g. clarifying
 XX gene function and screening drugs to regulate and treat the abnormal
 XX gene expression -
 XX Disclosure; Fig 5; 57pp; Japanese.
 XX The invention relates to a transgenic non-human mammal comprising at
 XX least one non-integrated transposon and/or at least one transposon
 XX signature site and/or a transposase gene in an expressible state. The
 XX invention also relates to methods of producing such transgenic non-human
 XX mammals, and also encompasses the selection of transgenic animals of the
 XX invention as disease models. The transgenic non-human mammals are used
 XX for elucidating gene function, in screening drugs to treat disorders of
 XX gene expression and protein function that are associated with disease,
 XX and as a source of organs for xenotransplantation into humans (e.g.,
 XX nerve cells, heart, lung, liver, spleen, kidney, cornea and skin).
 XX Sequences ABL55255-ABL55256 represent sequences which flank a
 XX Sleeping Beauty (SB) transposon in a vector (designated 1-8) used
 XX in the invention, and sequence ABL55257 represents the sequence
 XX that results after transposition of SB.
 XX Sequence 14 BP; 5 A; 2 C; 2 G; 5 T; 0 other;
 SQ Query Match 1.0%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 4.3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 2y 798 TTGCCATAAAGTCA 811
 14 TTGCCATAAAGTTA 1
 3B RESULT 708
 ID ABZ21280 standard; RNA; 14 BP.
 AC ABZ21280;
 DT 16-APR-2003 (first entry)
 DE FIXa aptamer oligonucleotide modulator, AS 3NT-3M, SEQ ID 39.
 XX Immunosuppressive; aptamer; infection; autoimmunity; tumour;
 KW inflammatory proliferative disease; hypoglycaemia; human;
 KW coagulation factor IXa; FIXa; ss.
 XX Unidentified.
 CS Key Location/Qualifiers
 PH modified_base 1..14
 FT /*tag= a
 FT /mod_base= "OTHER"
 FT /note= "All nucleotides are 2'Omethyl oligonucleotides"

XX WO200296926-A1.
 XX 05-DEC-2002.
 XX 28-MAY-2002; 2002WO-US16555.
 XX 25-MAY-2001; 2001US-293231P.
 XX 07-NOV-2001; 2001US-331037P.
 XX (UYDU-) UNIV DUKE.
 XX Sullenger BA, Rusconi C;
 XX WPI; 2003-140438/13.
 XX Altering affinity of nucleic acid ligands for target molecules in a
 XX patient or reversing binding of labeled ligands to target tissues, by
 XX administering (to a patient receiving the ligand) a modulator that
 XX binds to ligand -
 XX Claim 50; Page 74; 11pp; English.
 XX The present invention relates to a method for altering the affinity of a
 XX nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
 XX or in vitro, or reversing the binding of the labelled ligand to a target
 XX tissue. The method comprises administering a modulator that binds to the
 XX ligand to a patient receiving the ligand, or contacting the ligand with
 XX the modulator under conditions such that the modulator binds to the
 XX ligand, and thus alters the affinity of the ligand for the target
 XX molecule. The method is useful for treating a number of disorders e.g.
 XX infection, autoimmunity, tumours, inflammatory proliferative diseases and
 XX hypoglycaemia. The present sequence is an oligonucleotide modulator,
 XX which targets the FIXa aptamers 9.3t or 9.3t-3NT. The FIXa aptamers bind
 XX to human coagulation factor IXa and were used to illustrate the method of
 XX the invention. This oligonucleotide was found to be effective at
 XX reversing FIXa aptamer's anticoagulation activity in human plasma in
 XX vitro.
 XX Sequence 14 BP; 5 A; 2 C; 6 G; 1 U; 0 other;
 SQ Query Match 1.0%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 85.7%; Pred. No. 4.3e+02;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 971 GACATGTGGAGCA 984
 DB 1 GACATGTGGAGCA 14
 RESULT 709
 AAQ55455
 ID AAQ55455 standard; DNA; 15 BP.
 XX AAQ55455;
 AC AAQ55455;
 XX 25-MAR-2003 (updated)
 DT 19-JUL-1994 (first entry)
 DE Detection primer for cystic fibrosis mutation.
 XX Cystic fibrosis; CF; mutation; detection; primer extension; typing;
 KW genotype identification; biotinylated; ss.
 XX Synthetic.
 XX WO9401447-A1.
 XX 20-JAN-1994.
 XX 01-JUL-1993; 93WO-US06364.
 XX 02-JUL-1992; 92IL-0102382.


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27-JUL-1992; 92US-0919872.
(ERIP-) ERIPHYLE BV.
(FRIE/) FRIEDMAN M M.
Eyal N;
WPI; 1994-034981/04.
Determining identity of nucleotide base - by using primer
extension process, useful for typing of samples and genotype
identification
Example A; Page 24; 42pp; English.
The primers (AAQ55452-62) are use to detect mutations within the
cystic fibrosis gene. The primers are designed to be complementary
to eight of the most common mutations within the CF gene. Detection
is carried out by the incorporation of a labelled dideoxynucleotide.
Individuals carrying the mutation incorporate a different base as
opposed to normal individuals.
This primer detects the 551 mutation site by the
incorporation of ddTTP as opposed to ddCTP.
(Updated on 25-MAR-2003 to correct PN field.)
Sequence 15 BP; 2 A; 3 C; 3 G; 7 T; 0 other;
Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1438 TTCTGCTGCTGTTGA 1451
|||||||
2 TTCTGCTGCTGTTGA 15
RESULT 710
AAT56342
AAT56342 standard; RNA; 15 BP.
AAT56342;
25-MAR-2003 (updated)
14-MAY-1997 (first entry)
Mouse TNF-a hammerhead ribozyme target sequence (nt position 1315).
Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
intercellular adhesion molecule; rel A; tumour necrosis factor;
TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
translocation; chronic myelogenous leukaemia; CML; cancer;
Philadelphia chromosome; inflammation; autoimmune disease;
atherosclerosis; myocardial infarction; stroke; restenosis;
transplant rejection; rheumatoid arthritis; psoriasis;
myocardial ischaemia; Kawasaki disease; septic shock; HIV;
human immunodeficiency virus; acquired immune deficiency syndrome;
AIDS; Ss.
Mus musculus.
WO9523225-A2.
31-AUG-1995.
23-FEB-1995; 95WO-IB00156.
30-JAN-1995; 95US-0380734.
23-FEB-1994; 94US-0201109.
29-MAR-1994; 94US-0218934.
04-APR-1994; 94US-0222795.
07-APR-1994; 94US-0224483.
15-APR-1994; 94US-0227958.

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15-APR-1994; 94US-0228041.
18-MAY-1994; 94US-0245736.
06-JUL-1994; 94US-0271280.
15-AUG-1994; 94US-0281932.
16-AUG-1994; 94US-0291433.
17-AUG-1994; 94US-0292620.
19-AUG-1994; 94US-0293520.
02-SEP-1994; 94US-0300000.
08-SEP-1994; 94US-0303039.
23-SEP-1994; 94US-0311486.
23-SEP-1994; 94US-0311749.
28-SEP-1994; 94US-0314397.
03-OCT-1994; 94US-0316771.
07-OCT-1994; 94US-0319492.
11-OCT-1994; 94US-0321993.
04-NOV-1994; 94US-0334847.
10-NOV-1994; 94US-0337608.
28-NOV-1994; 94US-0345516.
16-DEC-1994; 94US-0357577.
23-DEC-1994; 94US-0363233.
(RIBO-) RIBOZYME PHARM INC.
Stinchcomb DT, Chowrita B, Drenzo A, Draper KG, Dudycz LM;
Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Meswigen JA;
Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
Thompson JD, Tracz D, Usman N, Wincott FE, Woolf I;
WPI; 1995-351090/45.
Ribozymes having modified bases and methods for producing them -
for use in inhibiting disease related genes
Claim 2; Page 252; 407pp; English.
The present sequence represents a preferred target sequence for an
enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
mRNA at the nucleotide base position indicated in the DE line.
Regions of the mRNA that do not form secondary folding
structures and that contain potential hammerhead and hairpin
CC ribozyme cleavage sites were identified by computer analysis.
CC Ribozymes directed against these mRNA sequences were designed and
CC synthesised with modifications that improve their nuclease
CC resistance. The ribozymes are designed to cleave the target
CC sequences and thereby inhibit TNF-alpha expression, making them
CC potentially useful for treating rheumatoid arthritis, septic shock
CC and other inflammatory disorders including psoriasis, as well as
CC for treatment of AIDS.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX Sequence 15 BP; 5 A; 0 C; 0 G; 10 U; 0 other;
SQ
Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 28.6%; Pred. No. 4.6e+02;
Matches 4; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
QY 1043 ATTATTTATGTTT 1056
|::|::|::|::|::|
DB 1 AUAUUAUUUAUU 14
RESULT 711
AAT54316
AAT54316 standard; RNA; 15 BP.
XX
XX AAT54316;
XX
XX 25-MAR-2003 (updated)
DT 24-MAR-1997 (first entry)
XX
XX Human IL-5 hammerhead ribozyme target sequence (nt. position 752).
XX
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX

```

gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
intercellular adhesion molecule; rel A; tumour necrosis factor;
TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
translocation; chronic myelogenous leukaemia; CML; cancer;
Philadelphia chromosome; inflammation; autoimmune disease;
atherosclerosis; myocardial infarction; stroke; restenosis;
transplant rejection; rheumatoid arthritis; psoriasis;
myocardial ischaemia; Kawasaki disease; septic shock; HIV;
human immunodeficiency virus; acquired immune deficiency syndrome;
AIDS; ss.

Homo sapiens.

WO9523225-A2.

31-AUG-1995.

23-FEB-1995; 95WO-IB00156.

30-JAN-1995; 95US-0380734.

23-FEB-1994; 94US-0201109.

29-MAR-1994; 94US-0218934.

04-APR-1994; 94US-0222795.

07-APR-1994; 94US-0224483.

15-APR-1994; 94US-0227958.

15-APR-1994; 94US-0228041.

18-MAY-1994; 94US-0245736.

06-JUL-1994; 94US-0271280.

15-AUG-1994; 94US-0291433.

16-AUG-1994; 94US-0291433.

17-AUG-1994; 94US-0292620.

19-AUG-1994; 94US-0293520.

02-SEP-1994; 94US-0300000.

08-SEP-1994; 94US-0303039.

23-SEP-1994; 94US-0311486.

23-SEP-1994; 94US-0311749.

28-SEP-1994; 94US-0314397.

03-OCT-1994; 94US-0316771.

07-OCT-1994; 94US-0319492.

11-OCT-1994; 94US-0321993.

04-NOV-1994; 94US-0334847.

10-NOV-1994; 94US-0337608.

28-NOV-1994; 94US-0345516.

16-DEC-1994; 94US-0357577.

23-DEC-1994; 94US-0363233.

(RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Chowrita B, Dizenzo A, Draper KG, Dudycz LW;

Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;

Modak A, Pavco P, Belgiman L, Sullivan SM, Sweedler D,

Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T,

WPI; 1995-351090/45.

Ribozymes having modified bases and methods for producing them -

for use in inhibiting disease related genes

Claim 2; Page 215; 407pp; English.

CC (related to parasitic infection or with pulmonary infiltration) and

CC L-tryptophan-associated eosinophilia-myalgia syndrome.

CC (Updated on 25-MAR-2003 to correct PI field.)

SQ Sequence 15 BP; 7 A; 0 C; 3 G; 5 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 15;

Best Local Similarity 71.4%; Pred. No. 4.6e+02;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Caps 0;

QY 1081 AAGAAATTGGAAA 1094

DB 2 AAGAAUUGGAAA 15

RESULT 712

RAAT54318

ID AAT54318 standard; RNA; 15 BP.

XX AC AAT54318;

XX 25-MAR-2003 (updated)

DT 24-MAR-1997 (first entry)

XX

DE Human IL-5 hammerhead ribozyme target sequence (nt. position 753).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;

XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;

XX intercellular adhesion molecule; rel A; tumour necrosis factor;

XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;

XX translocation; chronic myelogenous leukaemia; CML; cancer;

XX Philadelphia chromosome; inflammation; autoimmune disease;

XX atherosclerosis; myocardial infarction; stroke; restenosis;

XX transplant rejection; rheumatoid arthritis; psoriasis;

XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;

XX human immunodeficiency virus; acquired immune deficiency syndrome;

XX AIDS; ss.

XX Homo sapiens.

OS WO9523225-A2.

PN 31-AUG-1995.

PD 23-FEB-1995; 95WO-IB00156.

PF 30-JAN-1995; 95US-0380734.

PR 23-FEB-1994; 94US-0201109.

PR 29-MAR-1994; 94US-0218934.

PR 04-APR-1994; 94US-0222795.

PR 07-APR-1994; 94US-0224483.

PR 15-APR-1994; 94US-0227958.

PR 15-APR-1994; 94US-0228041.

PR 18-MAY-1994; 94US-0245736.

PR 06-JUL-1994; 94US-0271280.

PR 15-AUG-1994; 94US-0291433.

PR 16-AUG-1994; 94US-0291433.

PR 17-AUG-1994; 94US-0292620.

PR 19-AUG-1994; 94US-0293520.

PR 02-SEP-1994; 94US-0300000.

PR 08-SEP-1994; 94US-0303039.

PR 23-SEP-1994; 94US-0311486.

PR 23-SEP-1994; 94US-0311749.

PR 28-SEP-1994; 94US-0314397.

PR 03-OCT-1994; 94US-0316771.

PR 07-OCT-1994; 94US-0319492.

PR 11-OCT-1994; 94US-0321993.

PR 04-NOV-1994; 94US-0334847.

PR 10-NOV-1994; 94US-0337608.

PR 28-NOV-1994; 94US-0345516.

PR 16-DEC-1994; 94US-0357577.

PR 23-DEC-1994; 94US-0363233.

XX

(RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
Thompson JD, Tracz D, Usman N, Wincott PE, Woolf T;
WPI; 1995-351090/45.

Ribozymes having modified bases and methods for producing them -
for use in inhibiting disease related genes

Claim 2; Page 215; 407pp; English.

The present sequence represents a preferred target sequence for an
enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5
(IL-5) mRNA at the nucleotide base position indicated in the DE line.
Regions of the mRNA that do not form secondary folding
structures and that contain potential hammerhead and hairpin
ribozyme cleavage sites were identified by computer analysis.
Ribozymes directed against these mRNA sequences were designed and
synthesised with modifications that improve their nuclease
resistance. The ribozymes cleave the IL-5 target sequences and
thereby inhibit IL-5 expression, making them useful for treating
chronic asthma, e.g. by inhibiting the recruitment and activation of
lymphocytes and preventing the synthesis of IL-5 in
eosinophils. The ribozymes can also be used to treat eosinophilia
(related to parasitic infection or with pulmonary infiltration) and
L-tryptophan-associated eosinophilia-myalgia syndrome.
(Updated on 25-MAR-2003 to correct PI field.)

Sequence 15 BP; 7 A; 0 C; 3 G; 5 U; 0 other;
Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 4.6e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Y 1081 AAGAAATTGGAAAA 1094
b 1 AAGAAUUUGGUAAA 14

RESULT 713

AAT55821
D AAT55821 standard; RNA; 15 BP.
X C AAT55821;
X T 25-MAR-2003 (updated)
T 25-MAR-1997 (first entry)
X Human TNF-alpha hammerhead ribozyme target sequence (nt position 1276).
X Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
W gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
W intercellular adhesion molecule; rel A; tumour necrosis factor;
W TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
W translocation; chronic myelogenous leukaemia; CML; cancer;
W Philadelphia chromosome; inflammation; autoimmune disease;
W atherosclerosis; myocardial infarction; stroke; restenosis;
W transplant rejection; rheumatoid arthritis; psoriasis;
W myocardial ischaemia; Kawasaki disease; septic shock; HIV;
W human immunodeficiency virus; acquired immune deficiency syndrome;
W AIDS; ss.
X Homo sapiens.
X W09523225-A2.
X 31-AUG-1995.
X 23-FEB-1995; 95WO-IB00156.

30-JAN-1995; 95US-0380734.
PR 23-FEB-1994; 94US-0201109.
PR 29-MAR-1994; 94US-0218934.
PR 04-APR-1994; 94US-0222795.
PR 07-APR-1994; 94US-0224483.
PR 15-APR-1994; 94US-0227958.
PR 15-APR-1994; 94US-0228041.
PR 18-MAY-1994; 94US-0245736.
PR 06-JUL-1994; 94US-0271280.
PR 15-AUG-1994; 94US-0291932.
PR 16-AUG-1994; 94US-0291433.
PR 17-AUG-1994; 94US-0292620.
PR 19-AUG-1994; 94US-0293520.
PR 02-SEP-1994; 94US-0300000.
PR 08-SEP-1994; 94US-0303039.
PR 23-SEP-1994; 94US-0311486.
PR 23-SEP-1994; 94US-0311749.
PR 28-SEP-1994; 94US-0314397.
PR 03-OCT-1994; 94US-0316771.
PR 07-OCT-1994; 94US-0319492.
PR 11-OCT-1994; 94US-0321993.
PR 04-NOV-1994; 94US-0334847.
PR 10-NOV-1994; 94US-0337608.
PR 28-NOV-1994; 94US-0345516.
PR 16-DEC-1994; 94US-0357577.
PR 23-DEC-1994; 94US-0363233.
XX (RIBO-) RIBOZYME PHARM INC.
XX PA
XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
PI Thompson JD, Tracz D, Usman N, Wincott PE, Woolf T;
XX WPI; 1995-351090/45.
XX Ribozymes having modified bases and methods for producing them -
XX for use in inhibiting disease related genes
XX Claim 2; Page 243; 407pp; English.
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
XX mRNA at the nucleotide base position indicated in the DE line.
XX Regions of the mRNA that do not form secondary folding
XX structures and that contain potential hammerhead and hairpin
XX ribozyme cleavage sites were identified by computer analysis.
XX Ribozymes directed against these mRNA sequences were designed and
XX synthesised with modifications that improve their nuclease
XX resistance. The ribozymes are designed to cleave the target
XX sequences and thereby inhibit TNF-alpha expression, making them
XX potentially useful for treating rheumatoid arthritis, septic shock
XX and other inflammatory disorders including psoriasis, as well as
XX for treatment of AIDS.
XX (Updated on 25-MAR-2003 to correct PI field.)
XX Sequence 15 BP; 4 A; 1 C; 0 G; 10 U; 0 other;
SQ Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 28.6%; Pred. No. 4.6e+02;
Matches 4; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1045 TATTATGTATTATA 1058
Db 1 UAUTUAUUUAUUA 14

RESULT 714
AAT55803
ID AAT55803 standard; RNA; 15 BP.
XX AC
XX AC AAT55803;
XX

T 25-MAR-2003 (updated)
 T 25-MAR-1997 (first entry)
 X Human TNF-alpha hammerhead ribozyme target sequence (nt position 1263).
 X
 X Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 W gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 W intercellular adhesion molecule; rel A; tumour necrosis factor;
 W TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 W translocation; chronic myelogenous leukaemia; CML; cancer;
 W Philadelphia chromosome; inflammation; autoimmune disease;
 W atherosclerosis; myocardial infarction; stroke; restenosis;
 W transplant rejection; rheumatoid arthritis; psoriasis;
 W myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 W human immunodeficiency virus; acquired immune deficiency syndrome;
 W AIDS; ss.
 X
 X Homo sapiens.
 X
 N WO9523225-A2.
 N
 N 31-AUG-1995.
 N
 X 23-FEB-1995; 95WO-1B00156.
 X
 X 30-JAN-1995; 95US-0380734.
 X 23-FEB-1994; 94US-0201109.
 X 29-MAR-1994; 94US-0218934.
 X 04-APR-1994; 94US-0222795.
 X 07-APR-1994; 94US-0224483.
 X 15-APR-1994; 94US-0227958.
 X 18-APR-1994; 94US-0228041.
 X 06-JUL-1994; 94US-0245736.
 X 15-AUG-1994; 94US-0291932.
 X 16-AUG-1994; 94US-0291433.
 X 17-AUG-1994; 94US-0292620.
 X 19-AUG-1994; 94US-0293520.
 X 02-SEP-1994; 94US-0300000.
 X 08-SEP-1994; 94US-0303039.
 X 23-SEP-1994; 94US-0311486.
 X 28-SEP-1994; 94US-0311749.
 X 03-OCT-1994; 94US-0314397.
 X 07-OCT-1994; 94US-0316771.
 X 11-OCT-1994; 94US-0319492.
 X 04-NOV-1994; 94US-0321993.
 X 10-NOV-1994; 94US-0337608.
 X 28-NOV-1994; 94US-0345516.
 X 16-DEC-1994; 94US-0357577.
 X 23-DEC-1994; 94US-0363233.
 X
 X (RIBO-) RIBOZYME PHARM INC.
 X
 X Stinchcomb DT, Chowira B, Dhirenzo A, Draper KG, Dudycz LM;
 X Grimm S, Karpaisky A, Kisch K, Matulic-adamic J, Mcswiggen JA;
 X Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 X Thompson JD, Tracz D, Usman N, Wincott PE, Woolf T;
 X WPI; 1995-351090/45.
 X
 X Ribozymes having modified bases and methods for producing them -
 X for use in inhibiting disease related genes
 X
 X Claim 2; Page 243; 407pp; English.
 X
 X The present sequence represents a preferred target sequence for an
 X enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
 X mRNA at the nucleotide base position indicated in the DE line.
 X Regions of the mRNA that do not form secondary folding
 X structures and that contain potential hammerhead and hairpin
 X ribozyme cleavage sites were identified by computer analysis.
 X Ribozymes directed against these mRNA sequences were designed and

CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit TNF-alpha expression, making them
 CC potentially useful for treating rheumatoid arthritis, septic shock
 CC and other inflammatory disorders including psoriasis, as well as
 CC for treatment of AIDS.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 15 BP; 5 A; 0 C; 0 G; 10 U; 0 other;
 Query Match 1.0%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 28.6%; Pred. No. 4.6e+02;
 Matches 4; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
 QY 1043 ATTATTTATGTATT 1056
 Db 1 AUAUUUUUUUUUU 14
 RESULT 715
 AAT52043
 ID AAT52043 standard; RNA; 15 BP.
 XX
 AC AAT52043;
 XX
 DT 25-MAR-2003 (updated)
 DT 19-MAR-1997 (first entry)
 XX
 DE Human ICAM hammerhead ribozyme target sequence (nt. position 2158).
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 PF 23-FEB-1995; 95WO-1B00156.
 XX
 PR 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 18-APR-1994; 94US-0228041.
 PR 06-JUL-1994; 94US-0245736.
 PR 15-AUG-1994; 94US-0291932.
 PR 16-AUG-1994; 94US-0291433.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 08-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 28-SEP-1994; 94US-0311749.
 PR 03-OCT-1994; 94US-0314397.
 PR 07-OCT-1994; 94US-0316771.
 PR 11-OCT-1994; 94US-0319492.
 PR 04-NOV-1994; 94US-0321993.
 PR 10-NOV-1994; 94US-0337608.

[illegible]

23-DEC-1994; 94US-0363233.
(RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Chowira B, Dizenzo A, Draper KG, Dudycz LW, Grimm S, Karpeisky A, Kislich K, Matulic-adamic J, Meswigen JA, Modak A, Pavco P, Beigelman L, Sullivan SM, Sweedler D, Thompson JD, Tracz D, Usman N, Wincott FK, Woolf T; WPI; 1995-351090/45.

Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes
Claim 2; Page 180; 407pp; English.

The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with rheumatoid arthritis, asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to correct P1 field.)

Sequence 15 BP; 4 A; 0 C; 2 G; 9 U; 0 other;

Query Match	1.0%;	Score 12.4;	DB 1;	Length 15;
Best Local Similarity	28.5%;	Pred. No. 4.6e+02;		

1047 TTTATGTATT 1060
::|::|::|::
1 UUGAUGAUUUUU 14

SULT 719
66566/c
AAx66566 standard; RNA; 15 BP.
AAx66566:

20-JUL-1999 (first entry)
Human CD40 hammerhead ribozyme target SEQ ID NO:3198.

Arthritic condition; graft tolerance; immune response; target; cleavage; hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase; streptolysin; synovial membrane; joint; arthritis; osteoarthritis; rheumatoid arthritis; autoimmune disease; allergy; inflammation; diagnosis. ss.

Homo sapiens.

W09618736-A2

20-JUN-1996.

22-NOV-1995; 95WO-US15516.

05-OCT-1995; 95US-0541365;
13-DEC-1994; 94US-0354920.
23-DEC-1994; 94US-0363253.
23-DEC-1994; 94US-0363254.
17-FEB-1995; 95US-0390850.
20-APR-1995; 95US-0426124.
02-MAY-1995; 95US-0432874.
04-MAY-1995; 95US-0434509.

PR	07-JUL-1995;	95US-0000951.	
PR	07-JUL-1995;	95US-0000974.	
PR	07-AUG-1995;	95US-0512861.	
XX			(RIBO-) RIBOZYME PHARM INC.
XX			PA
XX			XX
PI			Draper K, Gustofson J, McSwiggen J, Pavco P, Stinchcomb DR;
PI			Beigelman L, Karpelsky A, Modak A, Usman N, Burgin A;
PI			Matulic-Adamic J, Jarvis T, Thompson JD, Wincott F;
XX			
XX			WPI; 1996-300653/30.
DR			
XX			
XX			
PT			Enzymatic nucleic acid molecules having a hammer-head motif - used
PT			for the treatment of arthritis, induction of graft tolerance or
PT			treatment of auto-immune diseases
XX			
XX			
PS			Claim 10; Page 204; 307pp; English.

The present invention describes a novel enzymatic nucleic acid (ENA) having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's can inhibit collagenase and stromelysin in the synovial membrane of joints for the treatment or prevention of arthritis, particularly osteoarthritis or rheumatoid arthritis. The ENA's can also be used to treat antigen presenting cells of a donor to induce tolerance in a recipient to an alloantigen of a donor. They can also be used for enhancing graft tolerance or for treating autoimmune disease, and for treating allergies and other inflammatory conditions. The ENA's can also be used in diagnosis. Ribozyme therapy impacts on the expression of stromelysin without introducing the non-specific effects upon gene expression which accompany treatment with retinoids and dexamethasone. The concentration of ribozyme required to affect a therapeutic treatment is lower than that required of antisense molecules, and is highly specific. The present sequence is used in the exemplification of the present invention.

Sequence 15 BP; 8 A; 3 C; 1 G; 3 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 1456 TGTTTATTATGTAC 1469
Db 15 TGTTTATTAGGTAC 2

RESULT 720
AAX65399/C
ID AAX65399 standard: RNA: 15 BP.

AA
AC AAX65399:

AA	DT	20-JUL-1999	(first entry)

XX
DE Mouse B7-1 hammerhead ribozyme target SEQ ID NO: 2031.

AA Arthritic condition; graft tolerance; immune response; target; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
 KW streptomycin; synovial membrane; joint; arthritis; osteoarthritis;
 KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
 KW diagnosis; ss.

XX
SO
OS

XX PN WO9618736-A2

XX
PD
20-JUN-1996

XX 22-NOV-1995: 95WO-US15516.

XX
PR 05-OCT-1995: 95US-0541365.

31-MAY-1996; 96SE-0002183.

(KUBI/) KUBISTA M.
(SVAN/) SVANVIK N.

Kubista M, Svanvik N;

WPI; 1998-032646/03.

Probe for target nucleic acid sequences - includes a reporter group whose signal properties are considerably altered when the probe binds to nucleic acid

Example 6; Page 21; 58pp; English.

This sequence is shown in the specification. The invention relates to a probe for target nucleic acid sequences, which comprises a sequence recognising element (SRE) covalently bound to a reporter group (RG) whose signal properties are considerably altered when it binds to nucleic acid (NA). The probe (i) at least in its part nearest to the RG, has a structure such that any intramolecular interaction between the SRE and RG is suppressed, or such that this intramolecular interaction minimally affects the signal properties, and/or (ii) upon binding to target sequences, creates a structure that increases the signal alteration caused by the binding of the RG to NA. Also claimed are three specific groups of asymmetric cyanine compounds which can be used as reporter groups in the above probe. The probes may be used for hybridisation to nucleic acids. They may be used for identification of specific genes, gene segments, RNA molecules and other nucleic acids. They may be used in clinical procedures, analysis of blood or urine, food technology, agriculture and biological research. They may be used, e.g. for identification of infectious diagnosis, or for testing the outcome of cloning procedures. The probes can be used in-vivo without damaging tissues or cells. They allow real time detection and can be used over a large temperature range.

Sequence 15 BP; 5 A; 4 C; 2 G; 4 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

458 TCACACTTCATGT 471

2 TCACACTGCATGT 15

SULT 723
X26372/C

AAK26372 standard; cDNA; 15 BP.

AAK26372;

26-MAY-1999 (first entry)

Antisense oligonucleotide directed against synthesis of duck HBV.

Antisense oligonucleotide; MuLV; membrane permeability; stability; DNA/RNA hybrid; ss.

Synthetic.

Duck hepatitis B virus.

Key Location/Qualifiers
misc_RNA 1..2 /*tag= a
misc_RNA 4..5 /*tag= b
misc_RNA 7 /*tag= c
misc_RNA 12 /*tag= d

XX

US5858988-A.

XX

12-JAN-1999.

XX

22-FEB-1996;

96US-0604871.

XX

22-FEB-1996;

96US-0604871.

XX

24-FEB-1993;

93US-0022055.

XX

23-FEB-1994;

94US-0200650.

XX

(WANG/) WANG J H.

XX

Wang JH;

XX

WPI; 1999-227825/19.

XX

Oligoribonucleotide conjugated at 2'-O position with modified phenyl

XX

Example 5; Column 25; 27pp; English.

XX

The present sequence represents an antisense oligonucleotide directed

XX

against synthesis of Duck Hepatitis B virus (HBV). The oligonucleotide

XX

was made to exemplify the invention. The specification describes an

XX

antisense oligoribonucleotide that is conjugated at the 2'-O position

XX

with a modified phenyl to produce a derivatized compound. The modified

XX

oligoribonucleotide can be used to enhance membrane permeability and

XX

stability and may also be used as an antisense therapeutic.

XX

Sequence 15 BP; 2 A; 4 C; 3 G; 6 U; 0 other;

XX

Query Match 1.0%; Score 12.4; DB 1; Length 15;

XX

Best Local Similarity 92.9%; Pred. No. 4.6e+02;

XX

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX

781 TCATGGGACATAA 794

XX

14 TCATGGGACAA 1

XX

RESULT 724

AAZ95561/c

XX

ID AAZ95561 standard; RNA; 15 BP.

XX

AAZ95561;

XX

06-JUN-2000 (first entry)

XX

Pyrene modified RNA oligonucleotide SEQ ID NO:1.

XX

Pyrene modified RNA; detection; hybridisation; uridine; ss.

XX

Synthetic.

XX

Key Location/Qualifiers

XX

modified_base 4 /*tag= a

XX

/note= "2'-O-(1-pyrenylmethyl)uridine"

XX

JP2000032999-A.

XX

02-FEB-2000.

XX

17-JUL-1998; 98JP-0202589.

XX

17-JUL-1998; 98JP-0202589.

XX

(TOAG) TOA GOSBI CHEM IND LTD.

XX

WPI; 2000-295685/26.

XX

A pyrene modified RNA and an analytical method of RNA -

XX

S Example 1; Page 10; 15pp; Japanese.

The present invention describes the detection of RNA with a hybridization assay using pyrene modified RNA. Where the RNA has a structural base sequence containing a base with introduced pyrene. The base with introduced pyrene in uridine residue; the uridine residue having a covalent bond with pyrene at 2'-OH. The hybridization assay for RNA can be used in a homogenous reaction system. It is the sensitive and simple detection of RNA. The present sequence represents a pyrene modified RNA oligonucleotide which is used in the exemplification of the present invention.

Sequence 15 BP; 4 A; 2 C; 4 G; 5 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 458 TCACACTTCATGT 471
D 14 TCACACTGCATGT 1

RESULT 725
AAZ95562/C
ID AAZ95562 standard; RNA; 15 BP.

XX AAZ95562;

XX 06-JUN-2000 (first entry)

XX Pyrene modified RNA oligonucleotide SEQ ID NO:2.

XX Pyrene modified RNA; detection; hybridisation; uridine; ss.

XX Synthetic.

XX Key Location/Qualifiers
XX modified_base 9
XX /tag= a
XX /note= "2'-O-(1-pyrenylmethyl)uridine"

XX JP2000032999-A.
XX 02-FEB-2000.

XX 17-JUL-1998; 98JP-0202589.

XX 17-JUL-1998; 98JP-0202589.

XX (TOAG) TOA GOSSEI CHEM IND LTD.

XX WPI; 2000-295685/26.

XX A pyrene modified RNA and an analytical method of RNA -
XX Example 1; Page 10; 15pp; Japanese.

XX The present invention describes the detection of RNA with a

XX hybridization assay using pyrene modified RNA. Where the RNA has a
XX structural base sequence containing a base with introduced pyrene.
XX The base with introduced pyrene in uridine residue; the uridine
XX residue having a covalent bond with pyrene at 2'-OH. The hybridization
XX assay for RNA can be used in a homogenous reaction system. It is the
XX sensitive and simple detection of RNA. The present sequence represents
XX a pyrene modified RNA oligonucleotide which is used in the
XX exemplification of the present invention.

XX Sequence 15 BP; 4 A; 2 C; 4 G; 5 U; 0 other;

XX Query Match 1.0%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 4.6e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 458 TCACACTTCATGT 471
DB 14 TCACACTGCATGT 1

RESULT 726
AAZ95563/C
ID AAZ95563 standard; RNA; 15 BP.

XX AAZ95563;

XX 06-JUN-2000 (first entry)

XX Pyrene modified RNA oligonucleotide SEQ ID NO:3.

XX Pyrene modified RNA; detection; hybridisation; uridine; ss.

XX Synthetic.

XX Key Location/Qualifiers
XX modified_base 11
XX /tag= a
XX /note= "2'-O-(1-pyrenylmethyl)uridine"

XX JP2000032999-A.
XX 02-FEB-2000.

XX 17-JUL-1998; 98JP-0202589.

XX 17-JUL-1998; 98JP-0202589.

XX (TOAG) TOA GOSSEI CHEM IND LTD.

XX WPI; 2000-295685/26.

XX A pyrene modified RNA and an analytical method of RNA -
XX Example 1; Page 11; 15pp; Japanese.

XX The present invention describes the detection of RNA with a
XX hybridization assay using pyrene modified RNA. Where the RNA has a
XX structural base sequence containing a base with introduced pyrene.
XX The base with introduced pyrene in uridine residue; the uridine
XX residue having a covalent bond with pyrene at 2'-OH. The hybridization
XX assay for RNA can be used in a homogenous reaction system. It is the
XX sensitive and simple detection of RNA. The present sequence represents
XX a pyrene modified RNA oligonucleotide which is used in the
XX exemplification of the present invention.

XX Sequence 15 BP; 4 A; 2 C; 4 G; 5 U; 0 other;

XX Query Match 1.0%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 4.6e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 458 TCACACTTCATGT 471
DB 14 TCACACTGCATGT 1

RESULT 727
AAZ95564/C
ID AAZ95564 standard; RNA; 15 BP.

XX AAZ95564;

XX 06-JUN-2000 (first entry)

XX Pyrene modified DNA/RNA oligonucleotide SEQ ID NO:4.

XX Pyrene modified RNA; detection; hybridisation; uridine; ss.

Q Sequence 15 BP; 4 A; 2 C; 4 G; 4 T; 1 U; 0 other;
 Query Match 1.0%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 4.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/ 458 TCAACACTTCATGT 471
 14 TCAACACTGCATGT 1

RESULT 730
 AZ39954/C
 D AAZ39954 standard; cDNA to mRNA; 15 BP.
 X
 C
 K AAZ39954;
 I 10-FEB-2000 (first entry)
 E Human interleukin-2 RNA probe L550A.
 K
 M Probe; higher-order structure; structure determination; RNA structure;
 W detection; human; interleukin-2; IL-2 RNA; ds.
 X
 S Synthetic.
 S Homo sapiens.
 N JP11285386-A.
 X
 D 19-OCT-1999.
 X
 F 03-APR-1998; 98JP-0091580.
 X
 R 03-APR-1998; 98JP-0091580.
 X
 A (BUNS-) BUNSHI BIOTONICS KENKYUSHO KK.
 X
 R WPI; 2000-026815/03.
 T Detection of the higher-order structure of an RNA - by hybridising with
 T a specific probe
 X
 S Example; Page 13; 26pp; Japanese.

X This sequence represents a probe for human interleukin-2 (IL-2) RNA.
 C The invention relates to a method for the detection of the higher-order
 C structure of an RNA, consisting of: (1) reacting the RNA with a probe
 C (P1) having a base sequence (B1) hybridisable with A1 among the specific
 C continuous base sequences A1 and A2 in the RNA and a probe (P2) having a
 C base sequence (B2) hybridisable with A2 among a specific continuous base
 C sequences A1 and A2 in the RNA; (2) detecting the continuous base
 C sequences B1 and B2 formed by hybridising the probes P1 and P2 on the
 C RNA; and (3) judging that: (i) the higher-order structure of the
 C specific continuous base sequences A1 and A2 in the RNA is
 C single-stranded when sequences B1 and B2 are detected; or (ii) the
 C higher-order structure of the specific continuous base sequences A1 and
 C A2 in the RNA is double-stranded when sequences B1 and B2 are not
 C detected. The method can also detect a change in the higher-order
 C structure of an RNA.

Q Sequence 15 BP; 9 A; 0 C; 0 G; 5 T; 1 other;
 Query Match 1.0%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 4.6e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1148 TTTATTTTATGATTT 1162
 15 TTTATTTTATGATTT 1

RESULT 731
 AAH20775/C

ID AAH20775 standard; DNA; 15 BP.
 XX
 AC AAH20775;
 DT 13-AUG-2001 (first entry)
 XX
 DE Complex PCR amplification type 1 primer #20.
 XX
 KW PCR primer; amplification; microarray; genotyping; mutational analysis;
 KW cytosine methylation pattern; ss.
 XX
 OS Unidentified.
 XX
 PN WO200136669-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 12-NOV-2000; 2000WO-DE03973.
 XX
 PR 12-NOV-1999; 99DE-1056203.
 PR 12-OCT-2000; 2000DE-1053714.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Berlin K;
 XX
 DR WPI; 2001-343834/36.
 XX
 PT Controlling performance of complex polymerase chain reaction
 PT amplification, useful e.g. for genotyping, using a set of many specific
 PT primers and non-specific counter-strand primers -
 XX
 PS Example 2; Page 17; 26pp; German.

XX This invention describes a novel controllable performance method of
 CC complex polymerase chain reaction (PCR) amplifications. Firstly, PCR is
 CC carried out with at least 50 different primers (P1) of one type, PCR
 CC complementary to one strand of sample DNA, and with a primer (or library
 CC of primers) of a second type (P2) complementary to the other strand of
 CC the DNA, with P2 carrying a marker (M1). Amplicons are hybridized either
 CC to an array of oligonucleotides (ON) that hybridize to the primer used
 CC for the first step, or to its complement, or to an array of ON
 CC complementary to the primers used in PCR, and then the lengths of
 CC amplicons bound to the array are determined using a second marker (M2).
 CC different from M1, that is correlated with the length of the relevant DNA
 CC fragments. Signals from M1 and M2 are quantified at relevant positions in
 CC the ON array. The method is used in whole genomic amplification for
 CC genotyping, mutational analysis or related applications, e.g. determining
 CC the cytosine methylation pattern of DNA. The method makes possible
 CC determination of the number and length of many different amplicons,
 CC something that is almost impossible when using two non-specific primers,
 CC as in the conventional method. AAH20756-AAH20823 represent the PCR
 CC primers used to illustrate the method of the invention.

XX Sequence 15 BP; 7 A; 0 C; 3 G; 5 T; 0 other;
 SQ
 Query Match 1.0%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 4.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1258 CAAATAATTTTITA 1271
 14 CAACTAATTTTITA 1

RESULT 732
 AAH20782
 ID AAH20782 standard; DNA; 15 BP.
 XX
 AC AAH20782;
 XX
 DT 13-AUG-2001 (first entry)
 XX

Complex PCR amplification type 1 primer #27.
 PCR primer; amplification; microarray; genotyping; mutational analysis;
 cytosine methylation pattern; ss.
 Unidentified.
 WO200136669-A2.
 25-MAY-2001.
 12-NOV-2000; 2000WO-DE03973.
 12-NOV-1999; 99DE-1056203.
 12-OCT-2000; 2000DE-1051714.
 (EPIG-) EPIGENOMICS AG.
 Berlin K;
 WPI; 2001-343834/36.
 Controlling performance of complex polymerase chain reaction
 amplification, useful e.g. for genotyping, using a set of many specific
 primers and non-specific counter-strand primers -
 Example 2; Page 17; 26pp; German.
 This invention describes a novel controllable performance method of
 complex polymerase chain reaction (PCR) amplifications. Firstly, PCR is
 carried out with at least 50 different primers (P1) of one type, and
 complementary to one strand of sample DNA, and with a primer (or library
 of primers) of a second type (P2) complementary to the other strand of
 the DNA, with P2 carrying a marker (M1). Amplicons are hybridized either
 to an array of oligonucleotides (ON) that hybridize to the primer used
 for the first step, or to its complement, or to an array of ON
 complementary to the primers used in PCR, and then the lengths of
 amplicons bound to the array are determined using a second marker (M2),
 different from M1, that is correlated with the length of the relevant DNA
 fragments. Signals from M1 and M2 are quantified at relevant positions in
 the ON array. The method is used in whole genomic amplification for
 genotyping, mutational analysis or related applications, e.g. determining
 the cytosine methylation pattern of DNA. The method makes possible
 determination of the number and length of many different amplicons,
 something that is almost impossible when using two non-specific primers,
 as in the conventional method. AAH20756-AAH20823 represent the PCR
 primers used to illustrate the method of the invention.
 Sequence 15 BP; 7 A; 0 C; 3 G; 5 T; 0 other;
 Query Match 1.0%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 4.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1086 TTTCGAAATAAGA 1099
 1 TTTCGAAATAATA 14
 SULT 733
 P98089/c
 AAF98089 standard; DNA; 15 BP.
 AAF98089;
 19-JUN-2001 (first entry)
 Human IGFA allele specific oligonucleotide probe SEQ ID NO:128.
 Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGFA;
 single nucleotide polymorphism; SNP; allele specific oligonucleotide;
 immunoassay; detection; PCR primer; probe; ss.

OS Homo sapiens.
 XX WO200111010-A2.
 XX 15-FEB-2001.
 XX 02-AUG-2000; 2000WO-US21097.
 XX 09-AUG-1999; 99US-0147860.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Chew A, Denton RR, Duda A, Kliem SE, Lanz EM, Mandabalan K;
 XX Stephens JC;
 XX WPI; 2001-202766/20.
 XX New polynucleotide for gene therapy, comprises nucleotide polymorphisms
 XX in the immunoglobulin E receptor I alpha subunit gene -
 XX Claim 15; Page 23; 99pp; English.
 XX The present invention describes an isolated polynucleotide (I) comprising
 XX a nucleotide sequence (S) which is a polymorphic variant of a reference
 XX sequence for the human immunoglobulin E receptor I alpha subunit (IGFA)
 XX gene or its fragment. The polymorphic variant comprises at least one
 XX polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,
 XX PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine
 XX (A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T)
 XX at PS4, PS8, PS16 or PS17, or (G) at a position corresponding to
 XX nucleotide 251, (A) at a position corresponding to nucleotide 302 or
 XX 741, and (T) at a position corresponding to nucleotide 530. (I) can be
 XX used in gene therapy. (I) is useful for therapeutic purposes. A
 XX polypeptide (II) encoded by (I) is useful in drug screening assays and
 XX in assays to measure the binding affinity of one or more candidate drugs
 XX targeting (II). An antibody (III) to (II) is useful to immunoprecipitate
 XX (II) from solution and also reacts with (II) on Western or immunoblots
 XX of polyacrylamide gels on membrane supports or substrates. (III) is also
 XX useful in immunoassays to detect (II) in biological samples. AAF97965 to
 XX AA98096 represent IGFA allele specific oligonucleotide probes; AAF98097
 XX to AA98140 represent IGFA gene polymorphism detection primers; and
 XX AAF98141 to AAF98180 represent IGFA gene PCR primers which are used in
 XX the exemplification of the present invention.
 XX Sequence 15 BP; 7 A; 4 C; 2 G; 2 T; 0 other;
 Query Match 1.0%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 4.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1346 TTGCAGCTGTGTT 1359
 Db 15 TTGCAGCTGTGTT 2
 RESULT 734
 AAF80981/c
 ID AAF80981 standard; DNA; 15 BP.
 XX AAF80981;
 AC AAF80981;
 XX 02-MAY-2001 (first entry)
 DT PTGS2 allele specific oligonucleotide primer SEQ ID 87.
 XX Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2;
 XX single nucleotide polymorphism; SNP; immune-related disorder; arthritis;
 XX inflammation; PCR primer; ss.
 OS Homo sapiens.
 XX WO200107662-A1.
 XX

21-JUN-2000; 2000WO-AU00693.

21-JUN-1999; 99US-0140345.

(MURD-) MURDOCH CHILDRENS RES INST.

Wraight CJ, Werther GA, Edmondson SR;

WPI; 2001-041421/05.

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisease nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation -

Example 7; Page 59; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisease oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisease oligonucleotides of the present invention (see AAF45151 and AAF45153-P45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia.

Sequence 15 BP; 3 A; 1 C; 0 G; 11 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1524 ATATTTTTAACTTT 1537

1 ATTTTAACTTT 14

SULT 737

F49026/c

AAF49026 standard; DNA; 15 BP.

AAF49026;

30-MAR-2001 (first entry)

IGFBP3 oligonucleotide #2446.

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cystostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

Homo sapiens.

WO200078341-A1.

28-DEC-2000.

21-JUN-2000; 2000WO-AU00693.

21-JUN-1999; 99US-0140345.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisease nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation -

XX Example 7; Page 60; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisease oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisease oligonucleotides of the present invention (see AAF45151 and AAF45153-P45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia.

XX Sequence 15 BP; 9 A; 0 C; 1 G; 5 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1038 TATTATTATTAT 1051

DB 15 TATTACTATTAT 2

RESULT 738

AAF49027/c

ID AAF49027 standard; DNA; 15 BP.

XX AAF49027;

XX 30-MAR-2001 (first entry)

XX IGFBP3 oligonucleotide #2447.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cystostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU00693.

XX 21-JUN-1999; 99US-0140345.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR;

X R WPI; 2001-041421/05.
 X T Ameliorating the effects of a disorder, e.g. psoriasis, by
 X T administering UV (ultra-violet) treatment (optional) and an antisense
 X T nucleic acid that inhibits or reduces growth factor mediated cell
 X T proliferation and/or inflammation -
 X S Example 7; Page 60; 201pp; English.
 X C The present invention relates to a method for ameliorating the effects
 X C of skin disorders. The method comprises contacting the skin with an
 X C antisense oligonucleotide, [for Insulin-like Growth Factor [IGF]-1
 X C receptor, IGF binding protein [IGFBP]-2 or IGFBP3], which is capable of
 X C inhibiting or reducing growth factor mediated cell proliferation,
 X C inflammation and/or other disorders. The present sequence is an
 X C oligonucleotide which can be used to design the antisense
 X C oligonucleotides of the present invention (see AAP45151 and
 X C AAP45153-P45161). The method is useful for ameliorating the effects of
 X C psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
 X C keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
 X C skin, a hyperneovascular condition such as a neovascular condition of the
 X C retina, brain or skin, growth factor-mediated malignancies, other
 X C sclerotic disease, kidney disease, hyperproliferation of the inside of
 X C blood vessels or any other hyperplasia.
 X C Sequence 15 BP; 10 A; 0 C; 1 G; 4 T; 0 other;
 Query Match 1.0%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 4.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Y 1038 TATTATTATTAT 1051
 b 14 TATTACTATTAT 1
 RESULT 739
 AC89686/c
 D ARC89686 standard; DNA; 15 BP.
 X C AC89686;
 X 13-MAR-2001 (first entry)
 X P. falciparum chitinase translation initiation site SEQ ID NO: 26.
 X Malaria; mosquito; chitinase; fungal disease; parasitic disease;
 X veterinary disease; arthropod pest; PCR primer; probe; ss.
 X Plasmodium falciparum.
 X WO200073488-A1.
 X 07-DEC-2000.
 X 26-MAY-2000; 2000WO-US14536.
 X 28-MAY-1999; 99US-0136508.
 X 03-FEB-2000; 2000US-0180051.
 X (TEXA) UNIV TEXAS SYSTEM.
 X Vinetz JM;
 X WPI; 2001-061553/07.
 X New nucleic acid encoding a plasmodium species chitinase is useful for
 X preventing transmission of malaria by mosquito feeding on subject that
 X may harbor Plasmodium species organisms -
 X Example 11; Page 133; 137pp; English.

CC The present invention provides the protein and coding sequences of the
 CC Plasmodium falciparum and P. gallinaceum chitinase enzymes. These
 CC organisms are the cause of malaria in humans. The sequences are useful
 CC in the prevention and treatment of malaria, fungal diseases, parasitic
 CC diseases and veterinary diseases, in preventing the transmission of
 CC malaria and in the control of arthropod pests in agriculture.
 CC Sequence 15 BP; 10 A; 1 C; 0 G; 4 T; 0 other;
 Query Match 1.0%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 4.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1047 TTTATGTTATTATT 1060
 Db 14 TTTATATATTATT 1
 RESULT 740
 ABX04022/c
 ID ABX04022 standard; DNA; 15 BP.
 X AC ABX04022;
 X 09-JAN-2003 (first entry)
 X Resistance gene linA DNA fragment.
 X Detection; probe; diagnosis; oral disease; paradontitis; caries; therapy;
 X polymorphism; virulence factor; antibiotic resistance gene; prognosis;
 X oral infection; detection; pathogen; coronary heart disease;
 X diabetic symptom; ss.
 X Unidentified.
 X DE20110013-U1.
 X 18-OCT-2001.
 X 13-MAR-2001; 2001DE-2010013.
 X 13-MAR-2001; 2001DE-2010013.
 X 13-MAR-2001; 2001DE-1012348.
 X (ROET/) ROETGER A.
 X Roetger A;
 X WPI; 2001-65777/76.
 X Oligonucleotide array, useful for diagnosing oral diseases,
 X particularly paradontitis, carries human or microbial reference
 X sequences -
 X Claim 10; Page 29; 58pp; German.
 X This invention describes a novel nucleotide carrier with probes used for
 X diagnosis of oral diseases, particularly paradontitis, but also caries,
 X especially to identify genetic predisposition (as indicated by
 X polymorphisms) to disease and to identify causative microorganisms or
 X their associated virulence factors and antibiotic resistance genes, e.g.
 X for selection of therapy and for prognosis. They are also useful for
 X research into oral infections. The carriers allow simultaneous detection
 X of both host and pathogen parameters, providing quickly and simply an
 X individual's paradontitis profile, including detection of pathogens that
 X are associated with increased risk of coronary heart diseases and/or
 X aggravation of diabetic symptoms, and of opportunistic pathogens.
 X CC ABX03670-ABX04044 represent DNA fragments used to illustrate the method
 X of the invention.
 X Sequence 15 BP; 2 A; 1 C; 7 G; 5 T; 0 other;
 Query Match 1.0%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

938 AGCCACCACTTAC 951
|||||
14 AGCCACCACTTAC 1

RESULT 741
U48101/c
AAL48101 standard; DNA; 15 BP.

AAL48101;
27-SEP-2002 (first entry)
Human neuropeptide Y allele specific primer SEQ ID NO: 25.
Human; neuropeptide Y; NPY; isogene; SNP; atherosclerosis; obesity;
psychological disorder; single nucleotide polymorphism; alcoholism;
antiarteriosclerotic; anorectic; PCR; primer; ss.
Homo sapiens.
WO200251857-A1.
04-JUL-2002.
21-DEC-2000; 2000WO-US34758.
21-DEC-2000; 2000WO-US34758.
(GENA-) GENAISSANCE PHARM INC.
Chew A, Denton RR, Lanz EM, Nandabalan K, Stephens JC;
WPI; 2002-566671/50.
New genetic variants of the human Neuropeptide Y (NPY) gene useful for
treating disorders affected by abnormal expression or function of NPY
isogene e.g., atherosclerosis or obesity -
Claim 11; Page 17; 80pp; English.
The present invention provides the human neuropeptide Y (NPY) gene and
single nucleotide polymorphisms (SNPs) identified therein. The sequence
can be used in the treatment of disorders associated with NPY, including
atherosclerosis, obesity, psychological disorders and alcoholism. The
present sequence is an allele specific primer used to isolate the human
NPY coding sequence.
Sequence 15 BP; 7 A; 5 C; 2 G; 1 T; 0 other;
Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1357 GTTGCTAGTCTGT 1370
|||||
15 GTTGCTAGTCTGT 2

RESULT 742
BK36967
ABK36967 standard; DNA; 15 BP.
ABK36967;
08-MAY-2002 (first entry)
Human ALAS2 gene allele-specific oligonucleotide probe #5.
Human; aminolevulinate delta synthase 2; ALAS2; haplotyping; primer; ss;

haplotype pair; single nucleotide polymorphism; genotyping; antianaemic;
gene therapy; drug screening; X-linked sideroblastic anaemia; sequencing;
hypochromic anaemia; probe; PCR.
Homo sapiens.
WO200210454-A2.
07-FEB-2002.
30-JUL-2001; 2001WO-US23914.
28-JUL-2000; 2000US-221827P.
(GENA-) GENAISSANCE PHARM INC.
Choi JY, Koshy B, Kliehm S, Stephens JC;
WPI; 2002-188755/24.
New isolated human aminolevulinate delta synthase 2 polynucleotide,
useful for therapeutic purposes, for studying the expression and
function of the polynucleotide, and for expressing the aminolevulinate
protein -
Claim 16; Page 13; 90pp; English.
The invention relates to single nucleotide polymorphisms in the gene
encoding human aminolevulinate delta synthase 2 (ALAS2). A method for
haplotyping the ALAS2 gene in an individual comprises identifying the
nucleotide at one or more polymorphic sites and determining whether one
of the copies of the gene is defined by one of the ALAS2 haplotypes given
in the specification or whether both copies are defined by a haplotype
pair. This method is useful in genotyping, whereby all possible haplotype
pairs can be assigned to specific genotypes. An association between a
trait and a haplotype or haplotype pair of the ALAS2 gene can be
identified by comparing the frequency of the haplotype or haplotype pair
in a population exhibiting the trait with the frequency of the haplotype
or haplotype pair in a reference population, where a higher haplotype
frequency in the trait population indicates the trait is associated with
the haplotype or haplotype pair. ALAS2 and its corresponding DNA are used
for studying the expression and function of ALAS2, for use in screening
for candidate drugs to treat diseases related to ALAS2 activity, such as
X-linked sideroblastic anaemia and hypochromic anaemia. The sequences are
also useful for studying the effect of variation on the biological
activity of ALAS2 as well as on the binding affinity of candidate drugs
targeting ALAS2. Sequences ABK36963-ABK37027 represent allele-specific
oligonucleotide probes, sequencing primers and PCR primers used to detect
ALAS2 gene polymorphisms.
Sequence 15 BP; 2 A; 4 C; 6 G; 2 T; 1 other;

Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

691 TTGGCCCAAGGCC 704
|||||
2 TTGGCCCAAGGCC 15

RESULT 743
ABL46363
IDL ABL46363 standard; DNA; 15 BP.
XX ABL46363;
XX ABL46363;
26-APR-2002 (first entry)
Human interferon gamma oligonucleotide SEQ ID NO:330.
Nucleic acid accessible hybridisation site; detection; hybridisation;
characterisation; identification; nucleic acid structure; diagnosis;

PCR primer; probe; ss.
Homo sapiens.
Synthetic.

WO200198537-A2.
27-DEC-2001.

15-JUN-2001; 2001WO-US19401.
17-JUN-2000; 2000US-212308P.
15-JUN-2001; 2001US-0212308.

(THIR-) THIRD WAVE TECHNOLOGIES INC.

Lyamichev V, Allawi H, Dong P, Neri BP, Vener IT;
WPI; 2002-049698/06.

Identifying oligonucleotides hybridizing to nucleic acids containing
secondary structure, useful in clinical diagnosis, comprises
identifying primers that interact with the target to form an extension
product under amplification conditions.

Claim 48; Fig 82A; 409pp; English.

The present invention describes a method for identifying oligonucleotides
with desired hybridisation properties to nucleic acid targets containing
secondary structure. The method comprises amplifying a target nucleic
acid having at least one accessible and one inaccessible site. Primers
that form an extension product are identified as the oligonucleotides
which can interact with the folded target nucleic acid. Oligonucleotides
from the present invention can be used in novel detection methods for
clinical diagnostic purposes, including the detection and identification
of pathogenic organisms (e.g. HIV). The method allows the ability to
rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
sequences used in the exemplification of the present invention.

Sequence 15 BP; 5 A; 2 C; 3 G; 5 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. NO. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1511 AATACAGGCTTTA 1524
2 ATTACAGGCTTTA 15

RESULT 744
AAD22543

AAD22543 standard; RNA; 15 BP.

AAD22543;

12-FEB-2002 (first entry)

Duck hepatitis B virus pre-S gene sense RNA fragment.

RNAse inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;
virucide; oncogene; cancer; transcription; translation; leukaemia virus;
human immunodeficiency virus; duck; hepatitis B virus; polymerase;
viral reverse transcriptase; pre-S gene; ss.

Duck hepatitis B virus.

US6291438-B1.

18-SEP-2001.

06-OCT-1998; 98US-0167375.

24-FEB-1993; 93US-0022055.
23-FEB-1994; 94US-0200650.
22-FEB-1996; 96US-0604871.

(WANG/) WANG J H.
Wang JH;

WPI; 2002-009339/01.

Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral
reverse transcriptase comprises at the 2'-O position of the
oligoribonucleotide, a hydrophobic carrier reagent containing a poly
substituted phenyl compound.

Claim 23; Column 37; 56pp; English.

The invention relates to derivatised antisense oligoribonucleotides with
enhanced membrane permeability and stability. The derivatised antisense
oligoribonucleotide complementary to a sequence of nucleotides found
in a virus or a cell is useful for inhibiting e.g., viral reverse
transcriptase. Derivatized antisense oligoribonucleotide is conjugated at
the 2'-O position with a hydrophobic carrier reagent containing a poly
substituted phenyl compound. The derivatised oligoribonucleotides are
used to decrease the expression of oncogenes and thereby decrease the
expression of cancer cells which rely upon oncogene expression for their
phenotypic and pathological properties. The oligoribonucleotides are also
used for increasing the effectiveness of antisense oligonucleotide
targeted to a gene associated with a disease or a condition in an
animal. To alter gene transcription and/or translation for any gene or
gene segment responsible for expression, to inhibit viral reverse
transcriptase, to inhibit the expression of leukaemia virus, hepatitis
virus, oncogenes and human immunodeficiency virus. The present sequence
is duck hepatitis B virus pre-S gene sense RNA fragment used in the
treatment of duck hepatitis B virus.

Sequence 15 BP; 6 A; 3 C; 4 G; 2 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. NO. 4.6e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

781 TGNATGGACAAATAA 794
2 UGAUGGGACACAA 15

OY

Db

RESULT 745

AAD22544/c

AAD22544 standard; RNA; 15 BP.

AAD22544;

12-FEB-2002 (first entry)

Duck hepatitis B virus pre-S gene antisense RNA fragment.

RNAse inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;
virucide; oncogene; cancer; transcription; translation; leukaemia virus;
human immunodeficiency virus; duck; hepatitis B virus; polymerase;
viral reverse transcriptase; pre-S gene; antisense; ss.

Duck hepatitis B virus.

US6291438-B1.

18-SEP-2001.

06-OCT-1998; 98US-0167375.

24-FEB-1993; 93US-0022055.

23-FEB-1994; 94US-0200650.

22-FEB-1996; 96US-0604871.

(WANG/) WANG J H.

Wang JH;

WPI; 2002-009339/01.

Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral reverse transcriptase comprises at the 2'-O position of the oligoribonucleotide, a hydrophobic carrier reagent containing a poly substituted phenyl compound -

Claim 23; Column 37; 56pp; English.

The invention relates to derivatised antisense oligoribonucleotides with enhanced membrane permeability and stability. The derivatised antisense oligoribonucleotide complementary to a sequence of nucleotides found in a virus or a cell is useful for inhibiting e.g., viral reverse transcriptase. Derivatized antisense oligoribonucleotide is conjugated at the 2'-O position with a hydrophobic carrier reagent containing a poly substituted phenyl compound. The derivatised oligoribonucleotides are used to decrease the expression of oncogenes and thereby decrease the expression of cancer cells which rely upon oncogene expression for their phenotypic and pathological properties. The oligoribonucleotides are also used for increasing the effectiveness of antisense oligonucleotide targeted to a gene associated with a disease or a condition in an animal. To alter gene transcription and/or translation for any gene or gene segment responsible for expression, to inhibit viral reverse transcriptase, to inhibit the expression of leukaemia virus, hepatitis virus, oncogenes and human immunodeficiency virus. The present sequence is duck hepatitis B virus pre-S gene antisense RNA fragment used in the treatment of duck hepatitis B virus.

Sequence 15 BP; 2 A; 4 C; 3 G; 6 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

781 TGATGGGACAAATAA 794
|||||
14 TGATGGGACAAACAA 1

SULT 746
X79855

ABX79855 standard; cDNA; 15 BP.

ABX79855;

17-APR-2003 (first entry)

EST polymorphic DNA repeat polymucleotide #180.

EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPOUS; Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

Homo sapiens.

US6472154-B1.

29-OCT-2002.

31-DEC-1999; 99US-0475947.

31-DEC-1999; 99US-0475947.

(TEXA) UNIV TEXAS SYSTEM.

Garner HR, Wren JD, Minna JD, Fondon JW;

WPI; 2003-208818/20.

Identifying a candidate polymorphic repeat within a coding sequence, for understanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability -

Examples; Column 835; 58pp; English.

The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia, myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTs.

Sequence 15 BP; 2 A; 5 C; 4 G; 4 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

402 CTCGTGCGTATCCA 415
|||||
1 CTCGTGCGCATCCA 14

RESULT 747

ABV93501

ID ABV93501 standard; DNA; 15 BP.

AC ABV93501;

08-JAN-2003 (first entry)

Bacillus thuringiensis toxin Cry mutant oligonucleotide #24.

Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site; pepsin; PCS; ss.

Bacillus thuringiensis.
Synthetic.

FR2822157-A1.

20-SEP-2002.

19-MAR-2001; 2001FR-0003691.

19-MAR-2001; 2001FR-0003691.

(AVET) AVENTIS CROPS SCIENCE SA.

Freyssinet G, Rang C, Frutos R;

WPI; 2003-002439/01.

New modified Cry protein, useful as insecticide, comprises at least one additional pepsin cleavage site to reduce persistence in mammalian gut

Example 3; Page 27; 134pp; French.

The present invention describes a modified Cry protein (I) that is sensitive to pepsin and comprises at least one additional pepsin cleavage site (PCS). Also described: (a) increasing pepsin sensitivity of Cry proteins by incorporating at least one extra PCS; (b) polynucleotides (ii) that encode (I); (c) chimeric genes (CG) that contain a promoter, (II) and terminator; (d) expression or transformation vector (III) that contains CG; (e) host organism (IV) transformed with (III), also, where the organism is a plant, its parts and seeds; (f) production of (I) by growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed against (I). (I) has insecticidal activity. (I) can be used as insecticides, particularly where expressed in transgenic plants, (I) are sensitive to enzymes in the digestive tract of mammals, so do not persist in the tract (lack of persistence is required by regulatory authorities for use, in foods, of seeds containing Cry proteins). Extra PCS do not increase degradation in the digestive tract of insects, so have no effect on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308 represent sequences used in the exemplification of the present invention.

Sequence 15 BP; 7 A; 0 C; 1 G; 7 T; 0 other;
Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 1392 TTAGAACTATTAAA 1405
b 1 TTAGAACTATTAAA 14

RESULT 748
BVP93785
D ABV93785 standard; DNA; 15 BP.
X C ABV93785;
X T 08-JAN-2003 (first entry)
X B. thuringiensis toxin Cry oligonucleotide mutant #24 SEQ ID NO:36.
X Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
X pepsin; PCS; ss.
X Bacillus thuringiensis.
X Synthetic.
X FR2822157-A1.
X 20-SEP-2002.
X 19-MAR-2001; 2001FR-0003691.
X 19-MAR-2001; 2001FR-0003691.
X (AVET) AVENTIS CROPS SCIENCE SA.
X Freyssonnet G, Raag C, Frutos R;
X WPI; 2003-002439/01.

New modified Cry protein, useful as insecticide, comprises at least one additional pepsin cleavage site to reduce persistence in mammalian gut
Disclosure; Page 106; 134pp; French.
The present invention describes a modified Cry protein (I) that is sensitive to pepsin and comprises at least one additional pepsin cleavage site (PCS). Also described: (a) increasing pepsin sensitivity of Cry proteins by incorporating at least one extra PCS; (b) polynucleotides (ii) that encode (I); (c) chimeric genes (CG) that contain a promoter, (II) and terminator; (d) expression or transformation vector (III) that contains CG; (e) host organism (IV) transformed with (III), also, where the organism is a plant, its parts and seeds; (f) production of (I) by

growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed against (I). (I) has insecticidal activity. (I) can be used as insecticides, particularly where expressed in transgenic plants. (I) are sensitive to enzymes in the digestive tract of mammals, so do not persist in the tract (lack of persistence is required by regulatory authorities for use, in foods, of seeds containing Cry proteins). Extra PCS do not increase degradation in the digestive tract of insects, so have no effect on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308 represent sequences used in the exemplification of the present invention.

Sequence 15 BP; 7 A; 0 C; 1 G; 7 T; 0 other;
Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1392 TTAGAACTATTAAA 1405
Db 1 TTAGAACTATTAAA 14

RESULT 749
AAV49172/c
ID AAV49172 standard; DNA; 16 BP.
X AC AAV49172;
X AC 15-OCT-1998 (first entry)
X rb gene antisense oligonucleotide rb-N-120.
X rb gene; antisense oligonucleotide; modulate; gene expression; ss.
X Synthetic.
X Homo sapiens.
X BP856579-A1.
X 05-AUG-1998.
X 31-JAN-1997; 97EP-0101531.
X 31-JAN-1997; 97EP-0101531.
X (BIOG-) BIOGNOSTIK GBS BIOMOLEKULARE DIAGNOSTIK.
X Brysch W, Schlingensiepen K;
X WPI; 1998-400910/35.

Preparation of antisense oligonucleotide(s) which lack long runs of consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate growth of cells in culture
Example 7; Fig 9c; 286pp; English.
AAV49008-236 represent antisense oligonucleotides directed against the rb gene. Of these, only oligonucleotides AAV49008-52 resulted in effective downregulation of negative growth control by rb, while oligonucleotides AAV49052-236 had little effect. The oligonucleotides exemplify the invention. The specification describes oligonucleotides that contain 8-30 nucleotides, which contain at most 8 nucleotides that can each form three hydrogen bonds to cytosine; do not contain four consecutive nucleotides able to form three H-bonds each to four consecutive cytosines; do not contain two sequences of three consecutive nucleotides each able to form three H-bonds to three consecutive cytosines, and the ratio between residues able to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The oligonucleotides are used to modulate expression of genes, particularly the genes for p53, Erb-B2, JunB, JunD, TGF-beta 1 or beta 2 to control

proliferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The oligonucleotides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases of cancer or (targeting TGF) for stimulating the immune system.

Sequence 16 BP; 5 A; 0 C; 2 G; 9 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1204 ATTAACAAACAAA 1217
|||||||
14 ATTAACAAATCATA 1

SULT 750
V49081/c
AAV49081 standard; DNA; 16 BP.

AAV49081;

15-OCT-1998 (first entry)

rb gene antisense oligonucleotide rb-N-29.

rb gene; antisense oligonucleotide; modulate; gene expression; ss.

Synthetic.
Homo sapiens.
EP856579-Al.
05-AUG-1998.

31-JAN-1997; 97EP-0101531.

31-JAN-1997; 97EP-0101531.

(BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

Brysch W, Schlingensiepen K;
WPI; 1998-400910/35.

Preparation of antisense oligo:nucleotide(s) which lack long runs of consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate growth of cells in culture

Example 7; Fig 9a; 286pp; English.

AAV49008-236 represent antisense oligonucleotides directed against the rb gene. Of these, only oligonucleotides AAV49008-52 resulted in effective downregulation of negative growth control by rb, while oligonucleotides AAV49052-236 had little effect. The oligonucleotides exemplify the invention. The specification describes oligonucleotides that contain 8-30 nucleotides, which contain at most 8 nucleotides that can each form three hydrogen bonds to cytosine; do not contain four consecutive nucleotides able to form three H-bonds each to four consecutive cytosines; do not contain two sequences of three consecutive nucleotides each able to form three H-bonds to three consecutive cytosines, and the ratio between residues able to form two H-bonds each (2R) or three such bonds (3R) is given by $2R/3R = 0.33-0.72$. The oligonucleotides are used to modulate expression of genes, particularly the genes for p53, ErbB-2, junB, jund, TGF-beta 1 or beta 2 to control proliferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The oligonucleotides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases of cancer or (targeting TGF) for stimulating the immune system.

XX Sequence 16 BP; 8 A; 1 C; 1 G; 6 T; 0 other;
SQ

Query Match 1.0%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1171 TTTTATTAGATAAA 1184
|||||||
14 TTTTATTAGCTAAA 1

RESULT 751
AAV48657/c
ID AAV48657 standard; DNA; 16 BP.

XX AAV48657;

15-OCT-1998 (first entry)

junB gene antisense oligonucleotide JunB-N-43.

junB; jund; antisense oligonucleotide; modulate; gene expression; ss.

Synthetic.
Homo sapiens.
EP856579-Al.
05-AUG-1998.

31-JAN-1997; 97EP-0101531.

31-JAN-1997; 97EP-0101531.

(BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

Brysch W, Schlingensiepen K;
WPI; 1998-400910/35.

Preparation of antisense oligo:nucleotide(s) which lack long runs of consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate growth of cells in culture

Example 3; Fig 5b; 286pp; English.

AAV48564-708 represent antisense oligonucleotides directed against the junB and jund genes. Of these, only oligonucleotides AAV48565-614 resulted in effective downregulation of negative growth control by JunB or jund, while AAV48615-708 had little effect. The oligonucleotides exemplify the invention. The specification describes oligonucleotides that contain 8-30 nucleotides, which contain at most 8 nucleotides that can each form three hydrogen bonds to cytosine; do not contain four consecutive nucleotides able to form three H-bonds each to four consecutive cytosines; do not contain two sequences of three consecutive nucleotides each able to form three H-bonds to three consecutive cytosines, and the ratio between residues able to form two H-bonds each (2R) or three such bonds (3R) is given by $2R/3R = 0.33-0.72$. The oligonucleotides are used to modulate expression of genes, particularly the genes for p53, ErbB-2, junB, jund, TGF-beta 1 or beta 2 to control proliferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The oligonucleotides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases of cancer or (targeting TGF) for stimulating the immune system.

Sequence 16 BP; 9 A; 2 C; 1 G; 4 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2Y 1045 TATTATGATTTA 1058
16 TATTATGATTTA 3

Db

RESULT 753
LAS00453/C
ID AAS00453 standard; DNA; 16 BP.
AC AAS00453;
XX
XX
XX 15-MAY-2001 (first entry)
XX
XX Lactococcus lactis pyrG gene PCR primer SLH6.
XX
XX PyrG; cytidine triphosphate synthetase; CTP; pyrimidine metabolism; UTP;
XX bacteriophage resistant; lactic acid bacterial culture; starter culture;
XX food industry; feed product; dairy product; fermentation process;
XX probiotic; PCR primer; ss.
XX
XX Lactococcus lactis subsp. cremoris MGI1363.
XX
XX WO200114520-A2.
XX
XX 01-MAR-2001.
XX
XX 10-AUG-2000; 2000WO-DK00446.
XX
XX 19-AUG-1999; 99US-0377152.
XX
XX (CHRR-) CHR HANSEN AS.
XX
XX Wadskov-Hansen SLL, Hammer K, Martinussen J;
XX WPI; 2001-218434/22.
XX
XX Obtaining a derivative of Lactococcus lactis subspecies cremoris having
XX reduced susceptibility to a bacteriophage, useful in food and feed
XX manufacturing, comprises mutating a gene involved in pyrimidine
XX metabolism of a parent bacterium -
XX
XX Example 1; Page 20; 70pp; English.
XX
XX The present sequence for Lactococcus lactis pyrG gene PCR primer SLH6
XX is used in the PCR of Lactococcus lactis subspecies cremoris wild type
XX strain MGI1363 pyrG gene. The pyrG gene encodes for cytidine triphosphate
XX (CTP) synthetase which is involved in pyrimidine metabolism by converting
XX UTP to CTP. The wild type CTP synthetase is used to construct
XX bacteriophage resistant lactic acid mutants (AAU00432-AAU00434) that have
XX a reduced susceptibility towards attack by at least one kind of
XX bacteriophage comprising subjecting a population of parent lactic acid
XX bacterial cells, which are initially susceptible towards bacteriophage
XX attack, to mutation in a gene involved in the pyrimidine metabolism. The
XX lactic acid bacterial cultures which have significantly reduced
XX susceptibility towards bacteriophage attacks are useful as starter
XX cultures in the manufacture of food and feed products, e.g. dairy
XX products and in other food fermentation processes. These may also be used
XX as probiotics, which when ingested by humans or animals in the form of
XX viable cells confers good health conditions, e.g. by suppressing harmful
XX microorganisms in the gastrointestinal tract, by enhancing the immune
XX system, or by contributing to the digestion of nutrients. Another strain
XX of L. lactis, M393, is a leaky mutant for the pyrG gene (AAS00458) in
XX that these cells do not require cytidine for growth but have a reduced
XX susceptibility to bacteriophages.

XX
XX Sequence 16 BP; 8 A; 2 C; 3 G; 3 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1626 TTGTTGTCAAAGT 1639
14 TTGTTGTCAAAGT 1

Db

RESULT 753
ABL59924/C
ID ABL59924 standard; DNA; 16 BP.
XX
XX AC ABL59924;
XX
XX 22-JUL-2002 (first entry)
XX
XX Bsho insertion RESite oligonucleotide #1.
XX
XX RESite; related to empty site; identification; transposon; genotyping;
XX nucleic acid database; DNA fingerprinting; genetic engineering; MITE;
XX miniature inverted-repeat transposable element; mapping; ss.
XX Synthetic.
XX OS
XX WO200163540-A2.
XX
XX 30-AUG-2001.
XX
XX 26-FEB-2001; 2001WO-CA00251.
XX
XX 24-FEB-2000; 2000US-0184650.
XX
XX (UTMC-) UNIV MCGILL.
XX
XX Bureau T;
XX
XX WPI; 2001-565451/63.
XX
XX Determining a value indicating nucleic acid (NA) being a transposon
XX from NA database, by comparing target site NA and both leading and
XX trailing flanking region sequence between potential transposon and its
XX match -
XX
XX Disclosure; Fig 1B; 31pp; English.
XX
XX The present invention describes a method for determining a value
XX indicative of a nucleic acid (NA) sequence being a transposon (Tn), by
XX identifying the location in a NA database where a potential Tn (I) to be
XX identified may be found, selecting flanking region sequence (FRS) of (I),
XX searching the database for a match of the FRS, comparing a target site
XX NA sequence and both leading and trailing FRS between (I) and the match,
XX and determining value as result of previous step. The method can be used
XX for determining a value indicative of a NA sequence being a transposon.
XX The transposons identified by the method can be used to genotype a NA
XX sequence using PCR (polymerase chain reaction) or hybridisation based
XX protocols and sequences unique to the mined transposons. The transposons
XX can also be used in fingerprinting or linkage studies, isolation of novel
XX genes, producing mutated or knockout genes, and delivery of engineered
XX genes. A copia-like retro transposon, PDRI, is successfully used to study
XX polymorphisms. Miniature inverted-repeat transposable elements (MITEs)
XX are used in a novel technology called inter-MITE polymorphism as mapping
XX and fingerprinting tools in barley. The method is accurate, efficient,
XX and allows high throughput identification of transposons compared to the
XX use of standard genetic and molecular biological approaches. The
XX transposon sequences discovered by the method greatly outnumber all of
XX the plant transposon sequences previously reported. The present sequence
XX represents a Bsho insertion RESite (related to empty site)
XX oligonucleotide, which is used in the exemplification of the present
XX invention.

XX
XX Sequence 16 BP; 5 A; 2 C; 2 G; 7 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

798 TTGCATCAAGTCA 811
 |||||
 15 TTGCATCAAGTCA 2

SULT 754
 LS9944/C
 ABL59944 standard; DNA; 16 BP.

ABL59944;

22-JUL-2002 (first entry)

Basho insertion RESite oligonucleotide #21.

RESite; related to empty site; identification; transposon; genotyping;
 nucleic acid database; DNA fingerprinting; genetic engineering; MITF;
 miniature inverted-repeat transposable element; mapping; ss.

Synthetic.

WO200163540-A2.

30-AUG-2001.

26-FEB-2001; 2001WO-CR00251.

24-FEB-2000; 2000US-0184650.

(UYMC-) UNIV MCGILL.

Bureau T;

WPI; 2001-565451/63.

Determining a value indicating nucleic acid (NA) being a transposon
 from NA database, by comparing target site NA and both leading and
 trailing flanking region sequence between potential transposon and its
 match -

Disclosure; Fig 1B; 31pp; English.

The present invention describes a method for determining a value
 indicative of a nucleic acid (NA) sequence being a transposon (Tn), by
 identifying the location in a NA database where a potential Tn (i) to be
 identified may be found, selecting flanking region sequence (FRS) of (i),
 searching the database for a match of the FRS, comparing a target site
 NA sequence and both leading and trailing FRS between (i) and the match,
 and determining value as result of previous step. The method can be used
 for determining a value indicative of a NA sequence being a transposon.
 The transposons identified by the method can be used to genotype a NA
 sequence using PCR (polymerase chain reaction) or hybridisation based
 protocols and sequences unique to the mined transposons. The transposons
 can also be used in fingerprinting or linkage studies, isolation of novel
 genes, producing mutated or knockout genes, and delivery of engineered
 genes. A copia-like retro transposon, PDRI, is successfully used to study
 polymorphisms. Miniature inverted-repeat transposable elements (MITEs)
 are used in a novel technology called inter-MITE polymorphism as mapping
 and fingerprinting tools in barley. The method is accurate, efficient,
 and allows high throughput identification of transposons compared to the
 use of standard genetic and molecular biological approaches. The
 transposon sequences discovered by the method greatly outnumber all of
 the plant transposon sequences previously reported. The present sequence
 represents a Basho insertion RESite (related to empty site)
 oligonucleotide, which is used in the exemplification of the present
 invention.

Sequence 16 BP; 8 A; 0 C; 2 G; 6 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 16;
 Best Local Similarity 92.9%; Pred. No. 4.9e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 995 TTTCATCATACAT 1008
 |||||
 DB 15 TTTCATCATATAT 2

RESULT 755

AAK98508/C

XX AAK98508 standard; DNA; 16 BP.

AC AAK98508;

XX 16-APR-2002 (first entry)

XX Nucleic acid quantitative analysis probe #15.

XX Target detection; quantitative analysis; probe; medical diagnosis;
 XX forensics; bacterial screening; tissue typing; gene expression analysis;
 XX genotyping; ss.

OS Synthetic.

FE Key Location/Qualifiers

FT modified_base 16

FT /*tag= a

FT /mod_base= OTHER

FT /note= "C-terminal amide"

XX WO200202810-A2.

XX 10-JAN-2002.

XX 02-JUL-2001; 2001WO-EP07575.

XX 01-JUL-2000; 2000DE-1033334.

XX (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH.

XX Bickel R, Ehrlich R, Ellinger T, Brannantraut E, Kaiser T, Schulz T;
 XX Wagner G;

XX WPI; 2002-154760/20.

XX Determining targets by interaction with probe array, useful e.g. for
 XX diagnosis, based on detecting formation of precipitate at specific
 XX probe sites -

XX Example 3; Page 38; 92pp; German.

XX The present invention relates to a method for the qualitative and
 XX quantitative detection of targets in a sample by molecular interaction
 XX between the target and probes in an array. The method can be used to
 XX detect interactions between nucleic acids, antigens and antibodies or
 XX receptor and ligands, particularly in applications such as medical
 XX diagnosis, forensic science, bacterial screening, tissue typing for
 XX transplantation, monitoring gene expression, and genotyping. The present
 XX sequence is a probe used in the exemplification of the invention.

XX Sequence 16 BP; 4 A; 4 C; 4 G; 4 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 16;
 Best Local Similarity 92.9%; Pred. No. 4.9e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 819 CTGGAATCTCTGGA 832

DB 14 CCGGAATCTCTGGA 1

RESULT 756

AAQ78890/C

XX AAQ78890 standard; DNA; 17 BP.

AC AAQ78890;

X 25-MAR-2003 (updated)
 F 18-DEC-1995 (first entry)
 K Humicola grisea glucoamylase hybridization probe.
 K Glucoamylase; DNA probe; gene cloning; protein secretion; ss.
 K Synthetic.
 K EP625577-A1.
 K 23-NOV-1994.
 K 27-AUG-1986; 94EP-0201751.
 K 29-AUG-1985; 85US-0771374.
 R 07-JUL-1986; 86US-0882224.
 R 27-AUG-1986; 86EP-0306624.
 K (GENV) GENENCOR INT INC.
 A Berka RM, Cullen D, Gray GL, Hayenga KJ, Lawlis VB;
 I WPI; 1994-359750/45.
 X Vectors and DNA for expressing polypeptide(s) in filamentous fungi
 R - include secretory signal sequences that are native or foreign to
 T heterologous polypeptide(s), such as chymosin or glucoamylase.
 S Example 9A3; Page 22; 50pp; English.
 S The DNA probe and corresponding probes covering the degenerate
 S sites (AAQ7885-Q7889) correspond to amino acids 17-22 of the
 C H. grisea glucoamylase peptide GAI (AA62933), and are used as
 C hybridization probes to detect and isolate H. grisea glucoamylase
 C DNA in a Southern blot. Resulting genomic DNA fragments are
 C excised and cloned in plasmid pRSH1. This illustrates the main
 C claims of the patent, i.e. a vector containing (i) DNA encoding
 C a heterologous polypeptide (chymosin, prochymosin, preprochymosin,
 C Aspergillus niger glucoamylase, H. grisea glucoamylase, or Mucor
 C miehei carboxyl protease), and (ii) a secretory signal peptide,
 C and a filamentous fungus (Aspergillus, Trichoderma, Neurospora,
 C Podospora, Endothia, Mucor, Cochliobolus or Pyricularia, especially
 C A. nidulans, A. awamori or T. reesei) transformed with the vector
 C for recombinant protein (enzyme) production.
 C (Updated on 25-MAR-2003 to correct PF field.)
 C (Updated on 25-MAR-2003 to correct PR field.)
 X Sequence 17 BP; 11 A; 1 C; 0 G; 4 T; 1 other;
 Q Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.1e+02;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Y 1521 TTTATATTTTACTTT 1536
 ||||| :||
 Jb 17 TTTATATTTTATMTT 2
 RESULT 757
 AAX63796/C
 ID AAX63796 standard; RNA; 17 BP.
 K AAX63796;
 K 20-JUL-1999 (first entry)
 K Rabbit stromelysin hammerhead target SEQ ID NO:428.
 DE Arthritic condition; graft tolerance; immune response; target: cleavage;
 K hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
 K stromelysin; synovial membrane; joint; arthritis; osteoarthritis;

KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
 KW diagnosis; ss.
 OS Oryctolagus cuniculus.
 PN WO9618736-A2.
 XX 20-JUN-1996.
 XX 22-NOV-1995; 95WO-US15516.
 XX 05-OCT-1995; 95US-0541365.
 PR 13-DEC-1994; 94US-0354920.
 PR 23-DEC-1994; 94US-0363253.
 PR 23-DEC-1994; 94US-0363254.
 PR 17-FEB-1995; 95US-0390850.
 PR 20-APR-1995; 95US-0426124.
 PR 02-MAY-1995; 95US-0432874.
 PR 04-MAY-1995; 95US-0434509.
 PR 07-JUL-1995; 95US-0000951.
 PR 07-JUL-1995; 95US-0000974.
 PR 07-AUG-1995; 95US-0512861.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA Draper K, Gustofson J, McSwiggen J, Pavco P, Stinchcomb DT;
 PI Beigelman L, Karpeisky A, Modak A, Usman N, Burgin A;
 PI Matulic-Adamic J, Jarvis T, Thompson JD, Wincott F;
 XX WPI; 1996-300653/30.
 XX Enzymatic nucleic acid molecules having a hammer-head motif - used
 FT for the treatment of arthritis, induction of graft tolerance or
 FT treatment of auto-immune diseases
 XX Example 1; Page 153; 307pp; English.
 XX The present invention describes a novel enzymatic nucleic acid (ENA)
 CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose
 CC residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)
 CC at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.
 CC The ENA's can inhibit collagenase and stromelysin production in the
 CC synovial membrane of joints for the treatment or prevention of arthritis,
 CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
 CC be used to treat antigen presenting cells of a donor to induce tolerance
 CC in a recipient to an alloantigen of a donor. They can also be used for
 CC enhancing graft tolerance or for treating autoimmune disease, and for
 CC treating allergies and other inflammatory conditions. The ENA's can also
 CC be used in diagnosis. Ribozyme therapy impacts on the expression of
 CC stromelysin without introducing the non-specific effects upon gene
 CC expression which accompany treatment with retinoids and dexamethasone.
 CC The concentration of ribozyme required to affect a therapeutic treatment
 CC is lower than that required of antisense molecules, and is highly
 CC specific. The present sequence is used in the exemplification of the
 CC present invention.
 XX Sequence 17 BP; 12 A; 2 C; 1 G; 2 U; 0 other;
 SQ Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 826 TCCTGGATTTT 839
 ||||| :||
 Db 14 TCCTGGATTTT 1
 RESULT 758
 AAX75067/C
 ID AAX75067 standard; RNA; 17 BP.
 XX AAX75067;
 XX


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28-JUL-1999 (first entry)
Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #595.

Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
fms-like tyrosine kinase 1; kinase insert domain containing receptor;
foetal liver kinase 1; ss.

Mus sp.
WO9715662-A2.
01-MAY-1997.
25-OCT-1996; 96WO-US17480.
11-JAN-1996; 96US-0584040.
26-OCT-1995; 95US-0005974.
(CHIR ) CHIRON CORP.
(RIBO-) RIBOZYME PHARM INC.
Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
WPI; 1997-259017/23.
Nucleic acid molecule modulating VEGF receptor(s) gene expression or
mRNA stability - useful for treating e.g. tumour angiogenesis,
psoriasis, rheumatoid arthritis, etc., in a human patient
Claim 4; Page 173; 218pp; English.

The present invention describes nucleic acid molecules which modulate
the synthesis, expression and/or stability of a mRNA encoding 1 or more
receptors of vascular endothelial growth factor (VEGF). A patient
(preferably human) having a condition associated with the level of the
fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
be treated by administering the nucleic acid molecule or the expression
vector to the patient. AAX67275 to AAX75752 represent specific examples
of nucleic acid molecules from the present invention.

Sequence 17 BP; 0 A; 1 C; 3 G; 13 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

617 CAAAAAACACAAA 630
|||||
17 CAAAAAACACAAA 4

SULT 759
X75063/C
AAX75069 standard; RNA; 17 BP.
AAX75069;

28-JUL-1999 (first entry)
Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #597.

Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
fms-like tyrosine kinase 1; kinase insert domain containing receptor;
foetal liver kinase 1; ss.

Mus sp.

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XX WO9715662-A2.
PN
XX
PD
XX
PP
XX 01-MAY-1997.
XX 25-OCT-1996; 96WO-US17480.
PR 11-JAN-1996; 96US-0584040.
PR 26-OCT-1995; 95US-0005974.
XX
XX (CHIR ) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
DR
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
XX Claim 4; Page 173; 218pp; English.
PS
XX
XX The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 U; 0 other;
SQ

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 616 CAAAAAACACAAA 629
|||||
DB 14 CAAAAAACACAAA 1

RESULT 760
AAX74782
ID AAX74782 standard; RNA; 17 BP.
XX
XX AC AAX74782;
XX
XX 28-JUL-1999 (first entry)
XX
XX DE Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #310.
XX
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX OS Mus sp.
XX
XX FN WO9715662-A2.
XX
XX PD 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US17480.
XX
XX 11-JAN-1996; 96US-0584040.
XX 26-OCT-1995; 95US-0005974.
XX
XX (CHIR ) CHIRON CORP.
PA

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A (RIBO-) RIBOZYME PHARM INC.
 I Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 X WPI; 1997-259017/23.
 K Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 L mRNA stability - useful for treating e.g. tumour angiogenesis,
 P psoriasis, rheumatoid arthritis, etc., in a human patient
 K Claim 4; Page 164; 218pp; English.
 K The present invention describes nucleic acid molecules which modulate
 C the synthesis, expression and/or stability of a mRNA encoding 1 or more
 C receptors of vascular endothelial growth factor (VEGF). A patient
 C (preferably human) having a condition associated with the level of the
 C fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 C receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 C angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 C be treated by administering the nucleic acid molecule or the expression
 C vector to the patient. AAX67275 to AAX75752 represent specific examples
 C of nucleic acid molecules from the present invention.
 X Sequence 17 BP; 11 A; 4 C; 1 G; 1 U; 0 other;
 SQ Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 616 ACAAAAACACACAA 629
 Db 2 ACAAAUACACAA 15
 RESULT 761
 AAX72896/c
 D AAX72896 standard; RNA; 17 BP.
 X AAX72896;
 C 28-JUL-1999 (first entry)
 T Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #329.
 E Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 W flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 W tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 W fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 W foetal liver kinase 1; ss.
 X Mus sp.
 N WO9715662-A2.
 D 01-MAY-1997.
 F 25-OCT-1996; 96WO-US17480.
 X 11-JAN-1996; 96US-0584040.
 R 26-OCT-1995; 95US-0005974.
 X (CHIR) CHIRON CORP.
 A (RIBO-) RIBOZYME PHARM INC.
 X Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 P WPI; 1997-259017/23.
 X Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 X Claim 4; Page 133; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.
 XX Sequence 17 BP; 5 A; 5 C; 2 G; 5 U; 0 other;
 SQ Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 467 CATGTATTGTGTGG 480
 Db 14 CATGTAAATGTGTGG 1
 RESULT 762
 AAX71477
 ID AAX71477 standard; RNA; 17 BP.
 X AAX71477;
 C 28-JUL-1999 (first entry)
 T Human KDR VEGF receptor hammerhead ribozyme substrate #489.
 E Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 W flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 W tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 W fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 W foetal liver kinase 1; ss.
 X Homo sapiens.
 N WO9715662-A2.
 D 01-MAY-1997.
 F 25-OCT-1996; 96WO-US17480.
 X 11-JAN-1996; 96US-0584040.
 R 26-OCT-1995; 95US-0005974.
 X (CHIR) CHIRON CORP.
 A (RIBO-) RIBOZYME PHARM INC.
 X Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 P WPI; 1997-259017/23.
 X Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 X Claim 4; Page 111; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.

3 GUCUAUAGUACA 16

XX

XX

Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 fms-like tyrosine kinase 1; Kinase insert domain containing receptor;
 foetal liver kinase 1; ss.

Homo sapiens.

WO9715662-A2.

01-MAY-1997.

25-OCT-1996; 96WO-US17480.

11-JAN-1996; 96US-0584040.

26-OCT-1995; 95US-0005974.

(CHIR) CHIRON CORP.

(RIBO-) RIBOZYME PHARM INC.

Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;

WPI; 1997-259017/23.

Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 mRNA stability - useful for treating e.g. tumour angiogenesis,
 psoriasis, rheumatoid arthritis, etc., in a human patient

Claim 4; Page 74; 218pp; English.

The present invention describes nucleic acid molecules which modulate
 the synthesis, expression and/or stability of a mRNA encoding 1 or more
 receptors of vascular endothelial growth factor (VEGF). A patient
 (preferably human) having a condition associated with the level of the
 fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 be treated by administering the nucleic acid molecule or the expression
 vector to the patient. AAX67275 to AAX75752 represent specific examples
 of nucleic acid molecules from the present invention.

Sequence 17 BP; 5 A; 5 C; 2 G; 5 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;

Best Local Similarity 64.3%; Pred. No. 5.1e+02;

Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Y 980 AACCACTTTAAGTT 993

b 1 AAGCAGCUUUAAGCU 14

RESULT 766

AX69328
 D AAX69328 standard; RNA; 17 BP.

AX69328;

28-JUL-1999 (first entry)

Human flt1 VEGF receptor hammerhead ribozyme substrate #623.

Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 fms-like tyrosine kinase 1; Kinase insert domain containing receptor;
 foetal liver kinase 1; ss.

Homo sapiens.

WO9715662-A2.

01-MAY-1997.

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25-OCT-1996; 96WO-US17480.

11-JAN-1996; 96US-0584040.

26-OCT-1995; 95US-0005974.

(CHIR) CHIRON CORP.

(RIBO-) RIBOZYME PHARM INC.

Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;

WPI; 1997-259017/23.

Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 mRNA stability - useful for treating e.g. tumour angiogenesis,
 psoriasis, rheumatoid arthritis, etc., in a human patient

Claim 4; Page 65; 218pp; English.

The present invention describes nucleic acid molecules which modulate
 the synthesis, expression and/or stability of a mRNA encoding 1 or more
 receptors of vascular endothelial growth factor (VEGF). A patient
 (preferably human) having a condition associated with the level of the
 fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 be treated by administering the nucleic acid molecule or the expression
 vector to the patient. AAX67275 to AAX75752 represent specific examples
 of nucleic acid molecules from the present invention.

Sequence 17 BP; 5 A; 3 C; 3 G; 6 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;

Best Local Similarity 50.0%; Pred. No. 5.1e+02;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 714 TCCGACCTTTAATT 727

Db 1 UCCGAGUUUAAUU 14

RESULT 767

AX69088

ID AAX69088 standard; RNA; 17 BP.

AX69088;

28-JUL-1999 (first entry)

Human flt1 VEGF receptor hammerhead ribozyme substrate #383.

Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 fms-like tyrosine kinase 1; Kinase insert domain containing receptor;
 foetal liver kinase 1; ss.

Homo sapiens.

WO9715662-A2.

01-MAY-1997.

25-OCT-1996; 96WO-US17480.

11-JAN-1996; 96US-0584040.

26-OCT-1995; 95US-0005974.

(CHIR) CHIRON CORP.

(RIBO-) RIBOZYME PHARM INC.

Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;

WPI; 1997-259017/23.

Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient

Claim 4; Page 58; 218pp; English.

The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.

Sequence 17 BP; 11 A; 4 C; 1 G; 1 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

616 ACACAAACACACAA 629
|||||
2 ACACAAACACACAA 15

SULT 768

V97418
AAV97418 standard; RNA; 17 BP.

AAV97418;

17-MAR-1999 (first entry)

Human EGF-R target sequence nucleotide position 1577.

Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence; hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation; cancer; genetic drift; detection; mutation; ss.

Homo sapiens.

WO9833893-A2.

06-AUG-1998.

14-JAN-1998; 98WO-US00730.

04-DEC-1997; 97US-0985162.

31-JAN-1997; 97US-0036476.

(RIBO-) RIBOZYME PHARM INC.
(UYAS-) UNIV ASTON.

Akhtar S, Fell P, McSwiggen JA;

WPI; 1998-437449/37.

Enzymatic nucleic acids - which cleave RNA derived from an epidermal growth factor receptor, useful for inhibiting cell proliferation and for treating cancers

Claim 5; Page 72; 109pp; English.

The present invention describes enzymatic nucleic acid molecules (NAMS) which specifically cleave RNA derived from an epidermal growth factor receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090 represent specifically claimed target sequence from human EGF-R. AAV98044 to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and

CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR CC expression levels e.g. to inhibit cell proliferation in the prevention or CC treatment of cancers. The NAMS can also be used as diagnostic tools to CC examine genetic drift and mutations within diseased cells or to detect CC the presence of EGF-R RNA in a cell.

XX Sequence 17 BP; 8 A; 2 C; 3 G; 4 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 530 AATTTCAGTAACA 543
|||||
Db 4 AAUUCAGGAACA 17

RESULT 769

AAV95855/c
ID AAV95855 standard; RNA; 17 BP.

XX AAV95855;

DT 01-MAR-1999 (first entry)

XX Solanidine glucosyltransferase target sequence position 960.

XX Solanidine; glucosyltransferase; potato; citrate synthase; target;
KW hammerhead ribozyme; hairpin ribozyme; alkaloid biosynthesis;
KW flower formation; cleavage; solanaceous plant; ss.

XX Solanum tuberosum.

XX WO9832843-A2.

XX 30-JUL-1998.

PF 14-JAN-1998; 98WO-US00738.

PR 24-NOV-1997; 97US-0979416.

PR 28-JAN-1997; 97US-0036545.

PR 28-JAN-1997; 97US-0036599.

XX (RIBO-) RIBOZYME PHARM INC.

XX McSwiggen JA, Zwick MG;

XX WPI; 1998-427939/36.

XX New enzymatic nucleic acid(s) - useful for, e.g. reducing alkaloid biosynthesis or regulating flowering

XX Claim 13; Page 49; 79pp; English.

CC The present invention describes enzymatic nucleic acid molecules with CC RNA-cleaving activity (e.g. ribozymes) which are capable of modulating CC the expression of plant genes: (i) involved in biosynthesis of CC alkaloids; or (ii) involved in flower formation. AAV95982 to AAV96334, CC and AAV96335 to AAV96354 represent potato solanidine glucosyltransferase CC hammerhead and hairpin ribozymes, respectively. AAV95629 to AAV95981, CC and AAV96355 to AAV96734 represent potato solanidine glucosyltransferase CC target sequences. AAV96733 to AAV97170, and AAV97171 to AAV97195 CC represent potato citrate synthase hammerhead and hairpin ribozymes, CC respectively. AAV96735 to AAV96772, and AAV97196 to AAV97220 represent CC potato citrate synthase target sequences. Ribozymes of the present CC invention can be used to inhibit the synthesis of toxic alkaloids in CC solanaceous plants, particularly potato but also tomato, pepper, CC aubergine and datura or to inhibit flowering in potato, lettuce, spinach, CC cabbage, brussel sprouts, arugula, kale, collards, chard, beet, turnip, CC sweet potato and turf grass. Also the ribozymes can be used for RNA CC manipulation in the same way that restriction endonucleases are for DNA, CC as well as to examine genetic drift and mutations in plants and to

C detect specific RNA. The ribozymes can be targeted to specific genes or
 C to consensus sequences within a family of related genes, and being
 C catalytic need to be present at only very low concentrations.

X Sequence 17 BP; 4 A; 2 C; 4 G; 7 U; 0 other;
 Q Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 758 ATATTGAGCAGC 771
 b 16 ACATTGAGCAGC 3

RESULT 770
 AV95856/C
 D AAV95856 standard; RNA; 17 BP.

X AAV95856;
 T 01-MAR-1999 (first entry)
 X Solanidine glucosyltransferase target sequence position 961.
 X Solanidine; glucosyltransferase; potato; citrate synthase; target;
 W hammerhead ribozyme; hairpin ribozyme; alkaloid biosynthesis;
 M flower formation; cleavage; solanaceous plant; ss.
 M Solanum tuberosum.

S WO9832843-A2.
 N 30-JUL-1998.
 D 14-JAN-1998; 98WO-US00738.
 F 24-NOV-1997; 97US-0979416.
 R 28-JAN-1997; 97US-0036545.
 R 28-JAN-1997; 97US-0036599.

(RIBO-) RIBOZYME PHARM INC.

McSwiggen JA, Zwick MG;

WPI; 1998-427939/36.

New enzymatic nucleic acid(s) - useful for, e.g. reducing alkaloid
 biosynthesis or regulating flowering

Claim 13; Page 49; 79pp; English.

The present invention describes enzymatic nucleic acid molecules with
 RNA-cleaving activity (e.g. ribozymes) which are capable of modulating
 the expression of plant genes: (i) involved in biosynthesis of
 alkaloids; or (ii) involved in flower formation. AAV95982 to AAV96334,
 and AAV96335 to AAV96354 represent potato solanidine glucosyltransferase
 hammerhead and hairpin ribozymes, respectively. AAV95629 to AAV95981,
 and AAV96355 to AAV96734 represent potato solanidine glucosyltransferase
 target sequences. AAV96773 to AAV97170, and AAV97171 to AAV97195
 represent potato citrate synthase hammerhead and hairpin ribozymes,
 respectively. AAV96735 to AAV96772, and AAV97196 to AAV97220 represent
 potato citrate synthase target sequences. Ribozymes of the present
 invention can be used to inhibit the synthesis of toxic alkaloids in
 solanaceous plants, particularly potato but also tomato, pepper,
 aubergine and datura or to inhibit flowering in potato, lettuce, spinach,
 cabbage, brussels sprouts, arugula, kale, collards, chard, beet, turnip,
 sweet potato and turf grass. Also the ribozymes can be used for RNA
 manipulation in the same way that restriction endonucleases are for DNA,
 as well as to examine genetic drift and mutations in plants and to
 detect specific RNA. The ribozymes can be targeted to specific genes or
 to consensus sequences within a family of related genes, and being
 catalytic need to be present at only very low concentrations.

XX Sequence 17 BP; 4 A; 3 C; 4 G; 6 U; 0 other;
 SQ Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 758 ATATTGAGCAGC 771
 Db 15 ACATTGAGCAGC 2

RESULT 771
 AAV5890/C
 ID AAV5890 standard; DNA; 17 BP.

XX AAV5890;
 XX 20-JAN-1999 (first entry)
 DT Primer C5 for Cytochrome C551 I coding sequence.
 XX Cytochrome C551; vitamin C production; electron transfer mediator;
 XX aldehyde production; ketone production; carboxylic acid production;
 KW alcohol dehydrogenase; aldehyde dehydrogenase; PCR primer; ss.

XW Synthetic.
 XX Gluconobacter oxydans.
 OS EP869175-A2.
 XX 07-OCT-1998.

PF 27-MAR-1998; 98EP-0105608.

XX 04-APR-1997; 97EP-0105583.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Asakura A, Hoshino T, Shinjoh M, Tomiyama N;

XX WPI; 1998-508491/44.

XX New Gluconobacter cytochrome c551 polypeptides I and II - useful as
 PT electron transfer mediators and especially for producing vitamin C
 XX Example 2; Fig 2; 22pp; English.

XX This sequence is a primer for DNA encoding the Gluconobacter cytochrome
 CC C551 I of the invention. The cytochrome c551 I protein has: (a) a
 CC molecular weight of 17-20kDa; (b) an absorption spectrum (for reduced
 CC form) with alpha, beta and gamma peaks at 551, 522 and 417 nm
 CC respectively; (c) a haem content of about 1 mole/mole protein; and (d) an
 CC isoelectric point of about 3.95. The novel cytochrome c is especially
 CC useful for producing vitamin C, as it is an electron transfer mediator
 CC which improves production of aldehydes, ketones and carboxylic acids from
 CC corresponding substrates in the presence of alcohol dehydrogenase and
 CC aldehyde dehydrogenase enzymes (AldH). It especially improves production
 CC of 2-KGA (an intermediate of vitamin C) from L-sorbose or D-sorbose. It
 CC can also be used as a source for protein-protein conjugates such as
 CC AADH-cytochrome c551 to improve total electron transfer efficiency.

XX Sequence 17 BP; 8 A; 1 C; 1 G; 2 T; 5 other;

QY Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 68.8%; Pred. No. 5.1e+02;
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1036 CCTATTATATATATAT 1051

Db 16 CRTATTTTATTTTAT 1

RESULT 772
W58891
AAV58891 standard; DNA; 17 BP.
AAV58891;
20-JAN-1999 (first entry)
Primer C5R for Cytochrome C551 I coding sequence.
Cytochrome C551; vitamin C production; electron transfer mediator;
aldehyde production; ketone production; carboxylic acid production;
alcohol dehydrogenase; aldehyde dehydrogenase; PCR primer; ss.
Synthetic.
Gluconobacter oxydans.
EP869175-A2.
07-OCT-1998.
27-MAR-1998; 98EP-0105608.
04-APR-1997; 97EP-0105583.
(HOFF) HOFFMANN LA ROCHE & CO AG F.
Asakura A, Hoshino T, Shinjoh M, Tomiyama N;
WPI; 1998-508491/44.
New Gluconobacter cytochrome c551 polypeptides I and II - useful as
electron transfer mediators and especially for producing vitamin C
Example 2; Fig 2; 22pp; English.
This sequence is a primer for DNA encoding the Gluconobacter cytochrome
C551 I of the invention. The cytochrome C551 I protein has: (a) a
molecular weight of 17-20kDa; (b) an absorption spectrum (for reduced
form) with alpha, beta and gamma peaks at 551, 522 and 417 nm
respectively; (c) a haem content of about 1 mole/mole protein; and (d) an
isoelectric point of about 3.95. The novel cytochrome C is especially
useful for producing vitamin C, as it is an electron transfer mediator
which improves production of aldehydes, ketones and carboxylic acids from
corresponding substrates in the presence of alcohol dehydrogenase and
aldehyde dehydrogenase enzymes (ADH). It especially improves production
of 2-KGA (an intermediate of vitamin C) from L-sorbose or D-sorbose. It
can also be used as a source for protein-protein conjugates such as
AADR-cytochrome c551 to improve total electron transfer efficiency.
Sequence 17 BP; 2 A; 1 C; 1 G; 8 T; 5 other;
Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 5.1e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
1036 CCTATTATTATTAT 1051
2 CTTATTATTATTAT 17
RESULT 773
AA17432
AA17432 standard; RNA; 17 BP.
AA17432;
19-JUN-2000 (first entry)
Aryl hydrocarbon nuclear transport substrate sequence SEQ ID NO:658.
Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;

KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus sclerosus; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX Homo sapiens.
OS WO9950403-A2.
DN 07-OCT-1999.
PD 24-MAR-1999; 99WO-US06507.
XX 27-MAR-1998; 98US-0079678.
XX (RIBO-) RIBOZYME PHARM INC.
PA Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
PI WPI; 1999-591315/50.
XX Novel ribozymes for modulating the synthesis, expression and/or
PT stability of an mRNA encoding an angiogenic factors -
XX Claim 53; Page 79; 305pp; English.
PS The present invention describes enzymatic nucleic acid molecules with
CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19085
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberosus sclerosus, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3.
XX Sequence 17 BP; 7 A; 1 C; 5 G; 4 U; 0 other;
SQ Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 5.1e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 724 AATTTCAGGAATTG 737
DB 4 AAUUCAGGAUAUG 17
RESULT 774
AA20578
ID AAA20578 standard; RNA; 17 BP.
XX AAA20578;
XX 19-JUN-2000 (first entry)
DT

XX DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:3804.

XX AC Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;

XX AC integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;

XX AC hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;

XX AC ophthalmologic; antiinflammatory; antiarthritic; antiporiatic; ARMD;

XX AC dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;

XX AC age related macular degeneration; inflammation; neovascular glaucoma;

XX AC myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;

XX AC tubercous sclerosis; pot-wine stain; Sturge Weber syndrome;

XX AC Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX AC Homo sapiens.

XX AC WO9950403-A2.

XX AC 07-OCT-1999.

XX AC 24-MAR-1999; 99WO-US06507.

XX AC 27-MAR-1998; 98US-0079678.

XX AC (RIBO-) RIBOZYME PHARM INC.

XX AC Pavco PA, Roberts B, Jarvis T, Coeshott C, McSwiggen JA;

XX AC WPI; 1999-591315/50.

XX AC Novel ribozymes for modulating the synthesis, expression and/or

XX AC stability of an mRNA encoding an angiogenic factors -

XX AC Claim 55; Page 154; 305pp; English.

XX AC The present invention describes enzymatic cleave RNA molecules with

XX AC RNA cleaving activity, which specifically cleave RNA encoded by an aryl

XX AC hydrocarbon nuclear transport (ARNT) gene, an integrin subunit beta 3

XX AC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to

XX AC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,

XX AC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their

XX AC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to

XX AC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086

XX AC and AAA19155 to AAA19222 represent their corresponding target sequences;

XX AC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme

XX AC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and

XX AC AAA21596 to AAA21688 represent their corresponding target sequences;

XX AC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence

XX AC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to

XX AC AAA23422 represent their corresponding target sequences. The ribozymes of

XX AC the invention are used for modulating the synthesis, expression and/or

XX AC stability of an mRNA encoding angiogenic factor, especially ARNT,

XX AC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are

XX AC especially used to treat cancer, diabetic retinopathy, age related

XX AC macular degeneration (ARMD), inflammation, and arthritis, as well as

XX AC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,

XX AC angiofibroma of tubercous sclerosis, pot-wine stains, Sturge Weber

XX AC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,

XX AC and other syndromes and diseases related to the levels of ARNT, Tie-2,

XX AC integrin subunit alpha-6, or integrin subunit beta-3.

XX AC Sequence 17 BP; 4 A; 2 C; 2 G; 9 U; 0 other;

XX AC Query Match 1.0%; Score 12.4; DB 1; Length 17;

XX AC Best Local Similarity 28.6%; Pred. No. 5.1e+02;

XX AC Matches 4; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1149 TTATTTTAGATATT 1162

DB 4 UUAUUUGGAUUAU 17

RESULT 775

AAA20579

XX AC AAA20579 standard; RNA; 17 BP.

XX AC AAA20579;

XX AC 19-JUN-2000 (first entry)

XX AC Integrin alpha 6 subunit substrate sequence SEQ ID NO:3805.

XX AC Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;

XX AC integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;

XX AC hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;

XX AC ophthalmologic; antiinflammatory; antiarthritic; antiporiatic; ARMD;

XX AC dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;

XX AC age related macular degeneration; inflammation; neovascular glaucoma;

XX AC myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;

XX AC tubercous sclerosis; pot-wine stain; Sturge Weber syndrome;

XX AC Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX AC Homo sapiens.

XX AC WO9950403-A2.

XX AC 07-OCT-1999.

XX AC 24-MAR-1999; 99WO-US06507.

XX AC 27-MAR-1998; 98US-0079678.

XX AC (RIBO-) RIBOZYME PHARM INC.

XX AC Pavco PA, Roberts B, Jarvis T, Coeshott C, McSwiggen JA;

XX AC WPI; 1999-591315/50.

XX AC Novel ribozymes for modulating the synthesis, expression and/or

XX AC stability of an mRNA encoding an angiogenic factors -

XX AC Claim 55; Page 154; 305pp; English.

XX AC The present invention describes enzymatic cleave RNA molecules with

XX AC RNA cleaving activity, which specifically cleave RNA encoded by an aryl

XX AC hydrocarbon nuclear transport (ARNT) gene, an integrin subunit beta 3

XX AC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to

XX AC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,

XX AC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their

XX AC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to

XX AC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086

XX AC and AAA19155 to AAA19222 represent their corresponding target sequences;

XX AC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme

XX AC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and

XX AC AAA21596 to AAA21688 represent their corresponding target sequences;

XX AC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence

XX AC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to

XX AC AAA23422 represent their corresponding target sequences. The ribozymes of

XX AC the invention are used for modulating the synthesis, expression and/or

XX AC stability of an mRNA encoding angiogenic factor, especially ARNT,

XX AC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are

XX AC especially used to treat cancer, diabetic retinopathy, age related

XX AC macular degeneration (ARMD), inflammation, and arthritis, as well as

XX AC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,

XX AC angiofibroma of tubercous sclerosis, pot-wine stains, Sturge Weber

XX AC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,

XX AC and other syndromes and diseases related to the levels of ARNT, Tie-2,

XX AC integrin subunit alpha-6, or integrin subunit beta-3.

XX AC Sequence 17 BP; 3 A; 3 C; 2 G; 9 U; 0 other;

XX AC Query Match 1.0%; Score 12.4; DB 1; Length 17;

XX AC Best Local Similarity 28.6%; Pred. No. 5.1e+02;

XX AC Matches 4; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1149 TTATTTTAGATATT 1162

DB 4 UUAUUUGGAUUAU 17

RESULT 775

AAA20579


```
Best Local Similarity 28.6%; Pred. No. 5.1e+02;
Matches 4; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
```

1524 ATATTTTAACTTT 1537
ov

D^b 4 AUAUUUUUACUUU 17

AAA21204:

19-JUN-2000 (first entry)

Integrin alpha 6 subunit substrate sequence SEO ID NO:4430.

Human; aryl hydrocarbon nuclear transport; AHT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; anticatabolic; ophthalmologic; antiinflammatory; antiarthritic; antipapillary; ARMD; dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

WO9950403-A2.

07-OCT-1999.

24-MAR-1999: 99WO-US06507.

27-MAR-1998; 98US-0079678.

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts B, Jarvis T, Coeshott C, McSwiggan JA;

WPI: 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors -

Claim 55: Page 193: 305pp: English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086 and AAA19155 to AAA19222 represent their corresponding target sequences; AAA19223 to AAA20361 and AAA211501 to AAA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and AAA21596 to AAA21688 represent their corresponding target sequences; AAA1689 to AAA22475 and AAA233263 to AAA23342 represent ribozyme sequences for integrin subunit beta 3, and AAA242476 to AAA23262, AAA23343 to AAA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (AMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiodroma of tuberous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 3 A; 1 C; 2 G; 11 U; 0 other;

very Match 1.0%; Score 12.4; DB 1; Length 17;

CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angioblastoma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 CC Sequence 17 BP; 7 A; 2 C; 1 G; 7 U; 0 other;
 CC
 CC Query Match 1.0%; Score 12.4; DB 1; Length 17;
 CC Best Local Similarity 50.0%; Pred. No. 5.1e-02;
 CC Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC Y 1617 AAAATATATTTTGT 1630
 CC ||||| :||| :|||
 CC 4 AAAAUAAUUUUUGU 17
 CC
 CC RESULT 780
 CC AA21375/C
 CC D AAA21375 standard; RNA; 17 BP.
 CC X
 CC X AAA21375;
 CC X
 CC X 19-JUN-2000 (first entry)
 CC X
 CC X Integrin alpha 6 subunit substrate sequence SEQ ID NO:4601.
 CC X Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 CC X integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 CC X hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 CC X ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 CC X dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 CC X age related macular degeneration; inflammation; neovascular glaucoma;
 CC X myopic degeneration; psoriasis; verruca vulgaris; angioblastoma;
 CC X tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
 CC X Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 CC X Homo sapiens.
 CC X WO9950403-A2.
 CC X 07-OCT-1999.
 CC X 24-MAR-1999; 99WO-US06507.
 CC X 27-MAR-1998; 98US-0079678.
 CC X (RIBO-) RIBOZYME PHARM INC.
 CC X Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 CC X WPI; 1999-591315/50.
 CC X Novel ribozymes for modulating the synthesis, expression and/or
 CC X stability of an mRNA encoding an angiogenic factors -
 CC X Claim 55; Page 204; 305pp; English.
 CC X The present invention describes enzymatic nucleic acid molecules with
 CC X RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC X hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC X gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC X AAA17157 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC X and AAA17158 to AAA17560 and AAA17623 to AAA17684 represent their
 CC X corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC X AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC X and AAA19155 to AAA19222 represent their corresponding target sequences;

CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angioblastoma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 CC Sequence 17 BP; 7 A; 2 C; 1 G; 7 U; 0 other;
 CC
 CC Query Match 1.0%; Score 12.4; DB 1; Length 17;
 CC Best Local Similarity 92.9%; Pred. No. 5.1e-02;
 CC Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC Y 1617 AAAATATATTTTGT 1630
 CC ||||| :||| :|||
 CC 15 AAAATATATTTTGT 2
 CC
 CC RESULT 781
 CC AA21377
 CC D AAA21377 standard; RNA; 17 BP.
 CC X
 CC X AAA21377;
 CC X
 CC X 19-JUN-2000 (first entry)
 CC X
 CC X Integrin alpha 6 subunit substrate sequence SEQ ID NO:4603.
 CC X Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 CC X integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 CC X hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 CC X ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 CC X dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 CC X age related macular degeneration; inflammation; neovascular glaucoma;
 CC X myopic degeneration; psoriasis; verruca vulgaris; angioblastoma;
 CC X tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
 CC X Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 CC X Homo sapiens.
 CC X WO9950403-A2.
 CC X 07-OCT-1999.
 CC X 24-MAR-1999; 99WO-US06507.
 CC X 27-MAR-1998; 98US-0079678.
 CC X (RIBO-) RIBOZYME PHARM INC.
 CC X Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 CC X WPI; 1999-591315/50.
 CC X Novel ribozymes for modulating the synthesis, expression and/or
 CC X stability of an mRNA encoding an angiogenic factors -
 CC X Claim 55; Page 204; 305pp; English.
 CC X The present invention describes enzymatic nucleic acid molecules with
 CC X RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC X hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC X gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC X AAA17157 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC X and AAA17158 to AAA17560 and AAA17623 to AAA17684 represent their
 CC X corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC X AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC X and AAA19155 to AAA19222 represent their corresponding target sequences;

CC AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT.
 CC and AA17168 to AA17560 and AA17623 to AA17684 represent their
 CC corresponding target sequences; AA17685 to AA18385 and AA19087 to
 CC AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
 CC and AA19155 to AA19222 represent their corresponding target sequences;
 CC AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
 CC AA21596 to AA21688 represent their corresponding target sequences;
 CC AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequences
 CC for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
 CC AA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT.
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 CC
 XX Sequence 17 BP; 6 A; 1 C; 1 G; 9 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 42.9%; Pred. No. 5.1e+02;
 Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

2Y 1618 AAATATATTTTGT 1631

|||||:|:|:|:|:
 1 AAAGUAGUUGGU 14

3RESULT 782

AA21423

ID AA21423 standard; RNA; 17 BP.

XX AA21423;

19-JUN-2000 (first entry)

Integrin alpha 6 subunit substrate sequence SEQ ID NO:4649.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 hammerhead ribozyme; angiogenic factor; cycostatic; antidiabetic;
 ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 age related macular degeneration; inflammation; neovascular glaucoma;
 myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
 Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

XX WO9950403-A2.

PD 07-OCT-1999.

24-MAR-1999; 99WO-US06507.

27-MAR-1998; 98US-0079678.

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or
 stability of an mRNA encoding an angiogenic factors -

Claim 55; Page 207; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
 CC AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
 CC and AA17168 to AA17560 and AA17623 to AA17684 represent their
 CC corresponding target sequences; AA17685 to AA18385 and AA19087 to
 CC AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
 CC and AA19155 to AA19222 represent their corresponding target sequences;
 CC AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
 CC AA21596 to AA21688 represent their corresponding target sequences;
 CC AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequences
 CC for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
 CC AA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT.
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 CC
 XX Sequence 17 BP; 5 A; 0 C; 5 G; 7 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 57.1%; Pred. No. 5.1e+02;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1126 AAGATGTTTGT 1139

|||||:|:|:|:|:
 1 AAAGAUGUUGGU 14

RESULT 783

AA22694

ID AA22694 standard; RNA; 17 BP.

XX AA22694;

19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SEQ ID NO:5920.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 hammerhead ribozyme; angiogenic factor; cycostatic; antidiabetic;
 ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 age related macular degeneration; inflammation; neovascular glaucoma;
 myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
 Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

XX WO9950403-A2.

PD 07-OCT-1999.

24-MAR-1999; 99WO-US06507.

27-MAR-1998; 98US-0079678.

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;

WPI; 1999-591315/50.

(GENE-) GENE LOGIC.
 A Allen AP, Lawrence T, Lescallett JL, Olson SJ, Thurber DB;
 I White MB;
 X WPI; 1999-371141/31.
 R Detecting mutations in the BRCA2 gene
 F Claim 16; Page 70; 76pp; English.
 S This invention describes novel primers and probes (AAx78355-X78378)
 C which are used to detect novel mutations in the human BRCA2 gene at
 C nucleotide positions 2192, 3772, 5193, 5374, 6495 or 6903. The products
 C of the invention are used for detecting in an individual a predisposition
 C or higher susceptibility to cancers such as breast or ovarian cancer.
 C The invention describes a process for the accurate identification of
 C sequence variation in a BRCA2 polynucleotide and the identification
 C process includes allele-specific sequence based assays of known sequence
 C variations.
 X
 X Sequence 17 BP; 8 A; 0 C; 1 G; 8 T; 0 other;
 Q Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 ZY 1010 AATTATTTTCAGT 1023
 DB 17 AATTATTTTCAGT 4
 RESULT 786
 ID AAF02053 standard; DNA; 17 BP.
 AC AAF02053;
 DT 16-FEB-2001 (first entry)
 DE Hammerhead ribozyme substrate #348.
 XW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 OS Homo sapiens.
 PN WO200061729-A2.
 PD 19-OCT-2000.
 PF 11-APR-2000; 2000WO-US09721.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PI Blatt L, Zwick M, Pavco P, McSwiggen J;
 XX WPI; 2000-647423/62.
 CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
 CC useful for producing e.g. granulocyte colony stimulating factor
 CC protein, interferon alpha and erythropoietin -
 CC
 CC Claim 37; Page 63; 164pp; English.
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 CC
 CC Sequence 17 BP; 8 A; 0 C; 1 G; 8 T; 0 other;
 Q Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 ZY 1010 AATTATTTTCAGT 1023
 DB 17 AATTATTTTCAGT 4
 RESULT 786
 ID AAF02053 standard; DNA; 17 BP.
 AC AAF02053;
 DT 16-FEB-2001 (first entry)
 DE Hammerhead ribozyme substrate #348.
 XW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 OS Homo sapiens.
 PN WO200061729-A2.
 PD 19-OCT-2000.
 PF 11-APR-2000; 2000WO-US09721.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PI Blatt L, Zwick M, Pavco P, McSwiggen J;
 XX WPI; 2000-647423/62.
 CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
 CC useful for producing e.g. granulocyte colony stimulating factor
 CC protein, interferon alpha and erythropoietin -
 CC
 CC Claim 37; Page 63; 164pp; English.
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in

CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 XW Sequence 17 BP; 8 A; 1 C; 1 G; 7 T; 0 other;
 Q Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 ZY 1005 ACATATAATTATTT 1018
 DB 17 AAATATAATTATTT 4
 RESULT 787
 ID AAF02055 standard; DNA; 17 BP.
 AC AAF02055;
 DT 16-FEB-2001 (first entry)
 DE Hammerhead ribozyme substrate #350.
 XW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 OS Homo sapiens.
 PN WO200061729-A2.
 PD 19-OCT-2000.
 PF 11-APR-2000; 2000WO-US09721.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PI Blatt L, Zwick M, Pavco P, McSwiggen J;
 XX WPI; 2000-647423/62.
 CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
 CC useful for producing e.g. granulocyte colony stimulating factor
 CC protein, interferon alpha and erythropoietin -
 CC
 CC Claim 37; Page 63; 164pp; English.
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the CAAT Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.
 CC
 CC Sequence 17 BP; 6 A; 1 C; 1 G; 9 T; 0 other;
 Q Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 ZY 1004 AACATAAATTATTT 1017
 DB 14 AAATAAATTATTT 1
 RESULT 788
 ID AAF02358 standard; DNA; 17 BP.
 XX

AC AAF02358;
 CX 16-FEB-2001 (first entry)
 DE Hammerhead ribozyme substrate #653.
 EW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 FW interferon alpha; ss.
 IX Homo sapiens.
 NX WO200061729-A2.
 DX 19-OCT-2000.
 FX 11-APR-2000; 2000WO-US09721.
 RX 12-APR-1999; 99US-0129390.
 AX (RIBO-) RIBOZYME PHARM INC.
 IX Blatt L, Zwick M, Pavco P, McSwiggen J;
 RX WPI; 2000-647423/62.
 SX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 TX useful for producing e.g. granulocyte colony stimulating factor
 TX protein, interferon alpha and erythropoietin -
 SX Claim 37; Page 70; 164pp; English.
 CX The present invention relates to enzymatic and antisense nucleic acid
 CX molecules that act as inhibitors of the expression of repressor genes
 CX encoding the T2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CX transcription factor gene, IRF-2 and/or the CAAT Displacement
 CX Protein (CDP). Inhibition of the repressors removes prevents
 CX inhibition (and consequently increases expression of) genes involved in
 CX the production of erythropoietin, granulocyte colony stimulating factor
 CX protein and interferon alpha.
 CX Sequence 17 BP; 3 A; 3 C; 4 G; 7 T; 0 other;
 CX
 CX Query Match 1.0%; Score 12.4; DB 1; Length 17;
 CX Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 CX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CX
 CX / 497 CCAGATGCATACA 510
 CX |||||
 CX 17 CCAGATGCATATAA 4
 CX
 CX RESULT 789
 CX AAF02464/c
 CX AAF02464 standard; DNA; 17 BP.
 CX
 CX AAF02464;
 CX 16-FEB-2001 (first entry)
 CX Hammerhead ribozyme substrate #759.
 CX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 CX interferon alpha; ss.
 CX Homo sapiens.
 CX WO200061729-A2.
 CX 19-OCT-2000.
 CX 11-APR-2000; 2000WO-US09721.
 CX 12-APR-1999; 99US-0129390.

XX (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, Zwick M, Pavco P, McSwiggen J;
 XX WPI; 2000-647423/62.
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 XX useful for producing e.g. granulocyte colony stimulating factor
 XX protein, interferon alpha and erythropoietin -
 XX Claim 37; Page 73; 164pp; English.
 XX The present invention relates to enzymatic and antisense nucleic acid
 XX molecules that act as inhibitors of the expression of repressor genes
 XX encoding the T2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 XX transcription factor gene, IRF-2 and/or the CAAT Displacement
 XX Protein (CDP). Inhibition of the repressors removes prevents
 XX inhibition (and consequently increases expression of) genes involved in
 XX the production of erythropoietin, granulocyte colony stimulating factor
 XX protein and interferon alpha.
 XX Sequence 17 BP; 0 A; 2 C; 3 G; 12 T; 0 other;
 XX
 XX Query Match 1.0%; Score 12.4; DB 1; Length 17;
 XX Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 1207 AACCAACAAACAA 1220
 XX |||||
 XX 17 AACCAACAAACAA 4
 XX
 XX RESULT 790
 XX AAF02466/c
 XX ID AAF02466 standard; DNA; 17 BP.
 XX AC AAF02466;
 XX 16-FEB-2001 (first entry)
 XX Hammerhead ribozyme substrate #761.
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 XX interferon alpha; ss.
 XX Homo sapiens.
 XX WO200061729-A2.
 XX 19-OCT-2000.
 XX 11-APR-2000; 2000WO-US09721.
 XX 12-APR-1999; 99US-0129390.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, Zwick M, Pavco P, McSwiggen J;
 XX WPI; 2000-647423/62.
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 XX useful for producing e.g. granulocyte colony stimulating factor
 XX protein, interferon alpha and erythropoietin -
 XX Claim 37; Page 73; 164pp; English.
 XX The present invention relates to enzymatic and antisense nucleic acid
 XX molecules that act as inhibitors of the expression of repressor genes
 XX encoding the T2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 XX transcription factor gene, IRF-2 and/or the CAAT Displacement
 XX Protein (CDP). Inhibition of the repressors removes prevents
 XX inhibition (and consequently increases expression of) genes involved in
 XX the production of erythropoietin, granulocyte colony stimulating factor
 XX protein and interferon alpha.

C inhibition (and consequently increases expression of) genes involved in
 C the production of erythropoietin, granulocyte colony stimulating factor
 C protein and interferon alpha.

X Q Sequence 17 BP; 2 A; 2 C; 3 G; 10 T; 0 other;
 Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1205 TTAACAAACAAC 1218
 b 15 TGAACAAACAAC 2

RESULT 791

AAF03200
 D AAF03200 standard; DNA; 17 BP.

C AAF03200;

X 16-FEB-2001 (first entry)

Hammerhead ribozyme substrate #1495.

Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 interferon alpha; ss.

Homo sapiens.

WO200061729-A2.

19-OCT-2000.

11-APR-2000; 2000WO-US09721.

12-APR-1999; 99US-0129390.

(RIBO-) RIBOZYME PHARM INC.

Blatt L, Zwick M, Pavco P, McSwiggen J;

WPI; 2000-647423/62.

Enzymatic and antisense nucleic acid inhibition of repressor genes,
 useful for producing e.g. granulocyte colony stimulating factor
 protein, interferon alpha and erythropoietin -

Claim 37; Page 90; 164pp; English.

The present invention relates to enzymatic and antisense nucleic acid
 molecules that act as inhibitors of the expression of repressor genes
 encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 transcription factor gene, IRF-2 and/or the CAAT Displacement
 Protein (CDP). Inhibition of the repressors removes prevents
 inhibition (and consequently increases expression of) genes involved in
 the production of erythropoietin, granulocyte colony stimulating factor
 protein and interferon alpha.

Sequence 17 BP; 7 A; 2 C; 2 G; 6 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1502 GCATTTTAAATAC 1515

b 4 GCATTTGTAATAC 17

RESULT 792

AAF03201
 ID AAF03201 standard; DNA; 17 BP.

XX AAF03201;
 AC 16-FEB-2001 (first entry)
 DT Hammerhead ribozyme substrate #1496.
 DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XW Homo sapiens.
 XX WO200061729-A2.
 OS 19-OCT-2000.
 XX 11-APR-2000; 2000WO-US09721.
 PF 12-APR-1999; 99US-0129390.
 PR (RIBO-) RIBOZYME PHARM INC.
 PA Blatt L, Zwick M, Pavco P, McSwiggen J;
 PI WPI; 2000-647423/62.
 DR Enzymatic and antisense nucleic acid inhibition of repressor genes,
 useful for producing e.g. granulocyte colony stimulating factor
 protein, interferon alpha and erythropoietin -

Claim 37; Page 90; 164pp; English.

The present invention relates to enzymatic and antisense nucleic acid
 molecules that act as inhibitors of the expression of repressor genes
 encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 transcription factor gene, IRF-2 and/or the CAAT Displacement
 Protein (CDP). Inhibition of the repressors removes prevents
 inhibition (and consequently increases expression of) genes involved in
 the production of erythropoietin, granulocyte colony stimulating factor
 protein and interferon alpha.

Sequence 17 BP; 5 A; 3 C; 2 G; 7 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 5.1e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1502 GCATTTTAAATAC 1515

Db 1 GCATTTGTAATAC 14

RESULT 793

AAF03239/c
 ID AAF03239 standard; DNA; 17 BP.

AC AAF03239;

DT 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #1534.

Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 interferon alpha; ss.

Homo sapiens.

WO200061729-A2.

19-OCT-2000.

11-APR-2000; 2000WO-US09721.


```

PR 12-APR-1999; 99US-0129390.
XX (RIBO-) RIBOZYME PHARM INC.
XX Blatt L, Zwick M, Pavco P, McSwiggen J;
XX WPI; 2000-647423/62.
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor
XX protein, interferon alpha and erythropoietin -
XX Claim 37; Page 90; 164pp; English.
XX The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
XX transcription factor gene, IRP-2 and/or the CAAT Displacement
XX Protein (CDP). Inhibition of the repressors removes prevents
XX inhibition (and consequently increases expression of) genes involved in
XX the production of erythropoietin, granulocyte colony stimulating factor
XX protein and interferon alpha.
XX Sequence 17 BP; 10 A; 0 C; 3 G; 4 T; 0 other;
XX
XX Query Match 1.0%; Score 12.4; DB 1; Length 17;
XX Best Local Similarity 92.9%; Pred. No. 5.1e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Y 1520 CTTTATATTTTAA 1533
b 14 CTTTATATTTTAA 1
XX
XX RESULT 794
XX AF04948
D AAF04948 standard; DNA; 17 BP.
K AAF04948;
K 16-FEB-2001 (first entry)
K Hammerhead ribozyme substrate #2464.
K Ribozyme; erythropoietin; granulocyte colony stimulating factor;
K interferon alpha; ss.
K Homo sapiens.
K WO200061729-A2.
K 19-OCT-2000.
K 11-APR-2000; 2000WO-US09721.
K 12-APR-1999; 99US-0129390.
K (RIBO-) RIBOZYME PHARM INC.
K Blatt L, Zwick M, Pavco P, McSwiggen J;
K WPI; 2000-647423/62.
K Enzymatic and antisense nucleic acid inhibition of repressor genes,
K useful for producing e.g. granulocyte colony stimulating factor
K protein, interferon alpha and erythropoietin -
K Claim 4; Page 112; 164pp; English.
K The present invention relates to enzymatic and antisense nucleic acid
K molecules that act as inhibitors of the expression of repressor genes
K encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
K transcription factor gene, IRP-2 and/or the CAAT Displacement
K Protein (CDP). Inhibition of the repressors removes prevents
K inhibition (and consequently increases expression of) genes involved in
K the production of erythropoietin, granulocyte colony stimulating factor
K protein and interferon alpha.
K Sequence 17 BP; 10 A; 0 C; 3 G; 4 T; 0 other;
K
K Query Match 1.0%; Score 12.4; DB 1; Length 17;
K Best Local Similarity 92.9%; Pred. No. 5.1e+02;
K Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
K
Y 1520 CTTTATATTTTAA 1533
b 14 CTTTATATTTTAA 1
XX
XX RESULT 795
XX AAF05508
D AAF05508 standard; DNA; 17 BP.
K AAF05508;
K 16-FEB-2001 (first entry)
K Hammerhead ribozyme substrate #2727.
K Ribozyme; erythropoietin; granulocyte colony stimulating factor;
K interferon alpha; ss.
K Homo sapiens.
K WO200061729-A2.
K 19-OCT-2000.
K 11-APR-2000; 2000WO-US09721.
K 12-APR-1999; 99US-0129390.
K (RIBO-) RIBOZYME PHARM INC.
K Blatt L, Zwick M, Pavco P, McSwiggen J;
K WPI; 2000-647423/62.
K Enzymatic and antisense nucleic acid inhibition of repressor genes,
K useful for producing e.g. granulocyte colony stimulating factor
K protein, interferon alpha and erythropoietin -
K Claim 18; Page 118; 164pp; English.
K The present invention relates to enzymatic and antisense nucleic acid
K molecules that act as inhibitors of the expression of repressor genes
K encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
K transcription factor gene, IRP-2 and/or the CAAT Displacement
K Protein (CDP). Inhibition of the repressors removes prevents
K inhibition (and consequently increases expression of) genes involved in
K the production of erythropoietin, granulocyte colony stimulating factor
K protein and interferon alpha.
K Sequence 17 BP; 10 A; 0 C; 3 G; 4 T; 0 other;
K
K Query Match 1.0%; Score 12.4; DB 1; Length 17;
K Best Local Similarity 92.9%; Pred. No. 5.1e+02;
K Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
K
Y 829 TGGATTTTTCG 842
b 4 TGGATTTTTCG 17
XX
XX RESULT 796
XX AAF05509

```


KW tumour characterisation; hybridisation; ss.
 XX Homo sapiens.
 XX WO200018960-A2.
 XX 06-APR-2000.
 XX 24-SEP-1999; 99WO-US22283.
 XX 25-SEP-1998; 98US-0101757.
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX Landers JE, Jordan B, Housman DE, Charest A;
 XX WPI; 2000-293181/25.
 XX Detection of single nucleotide polymorphisms in genomes by preparation
 XX and analysis of reduced complexity genomes, useful for genotyping,
 XX fingerprinting and determining allele frequency of SNPs -
 XX Disclosure; Page 70; 11pp; English.
 XX A method has been developed for detecting the presence or absence of a
 XX single nucleotide polymorphism (SNP) allele in a genomic sample. The
 XX method comprises preparing a reduced complexity genome (RCG) from the
 XX genomic sample and analysing the RCG for the presence or absence of a
 XX SNP allele. The method can be used to characterise a tumour, to generate
 XX a genomic pattern for an individual genome or to generate a genomic
 XX classification code for a genome. The method can be used to assess
 XX whether a subject is at risk for developing a disease or to identify a
 XX set of SNP alleles associated with a disease. The method can also be
 XX used to perform linkage analysis. AAA3594 to AAA35947 represent
 XX sequences used in the exemplification of the present invention. AAA35948
 XX to AAA36632 represent nucleotide sequences containing SNPs.
 XX Sequence 17 BP; 5 A; 1 C; 5 G; 6 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1191 TCAGGGTTTAA 1204
 DB 4 TCAGGGTTTAA 17

RESULT 802
 ID AAA25555/c
 AC AAA25555 standard; DNA; 17 BP.
 AC AAA25555;

DT 19-JUL-2000 (first entry)
 XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2053.
 XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 XX gene expression modification; cancer; phosphorothioate; endonuclease;
 XX anticancer; breast cancer; endometrium cancer; ss.

OS Homo sapiens.
 XX WO9954459-A2.
 XX 28-OCT-1999.
 XX 19-APR-1999; 99WO-US08547.
 XX 20-APR-1998; 98US-0082404.
 XX 23-JUN-1998; 98US-0103636.

XX (RIBO-) RIBOZYME PHARM INC.
 XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
 XX Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
 XX Matulic-Adamic J;
 XX WPI; 2000-013248/01.
 XX New nucleic acids that interact, and optionally cleave, target
 XX sequences, used to treat cancer -
 XX Claim 77; Page 83; 149pp; English.

XX The present invention describes nucleic acids (A) that interact stably
 XX with a target sequence and contain at least one phosphorodithioate
 XX link, having endonuclease activity. (A), and more generally any
 XX catalytic nucleic acid (A') that modulates expression of the oestrogen
 XX receptor gene, are used to treat cancer (particularly of breast or
 XX endometrium), in vivo or by transforming cells ex vivo and implanting
 XX treated cells, or for other conditions associated with levels of
 XX oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 XX can also be used to correlate inhibition of gene expression with
 XX alterations in phenotype, particularly for identification of therapeutic
 XX targets, and as research reagents (for RNA, in the same way that
 XX restriction endonucleases are used with DNA). The combination of
 XX modifications in (A) improves resistance to nucleases, binding affinity
 XX and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
 XX hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 XX corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 XX receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 XX their corresponding target sequences. AAA26219 to AAA26271 represent
 XX other ribozyme sequences and antisense oligonucleotides used in the
 XX exemplification of the present invention.

XX Sequence 17 BP; 13 A; 1 C; 0 G; 3 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1143 TTTATTTTATTTA 1156
 DB 16 TTTGTTTATTTA 3

RESULT 803
 ID AAA25890
 AC AAA25890 standard; DNA; 17 BP.
 AC AAA25890;

DT 19-JUL-2000 (first entry)
 XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2388.
 XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 XX gene expression modification; cancer; phosphorothioate; endonuclease;
 XX anticancer; breast cancer; endometrium cancer; ss.

OS Homo sapiens.
 XX WO9954459-A2.
 XX 28-OCT-1999.
 XX 19-APR-1999; 99WO-US08547.
 XX 20-APR-1998; 98US-0082404.
 XX 23-JUN-1998; 98US-0103636.
 XX (RIBO-) RIBOZYME PHARM INC.

X Thompson JD, Beigelman L, McSwiggen JA, Karpetsky A, Bellon L;
 Y Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 b Matulic-Adamic J;
 WPI; 2000-013248/01.
 New nucleic acids that interact, and optionally cleave, target
 sequences, used to treat cancer -
 Claim 77; Page 93; 148pp; English.
 The present invention describes nucleic acids (A) that interact stably
 with a target sequence and contain at least one phosphorodithioate
 link, having endonuclease activity. (A), and more generally any
 catalytic nucleic acid (A') that modulates expression of the oestrogen
 receptor gene, are used to treat cancer (particularly of breast or
 endometrium), in vivo or by transforming cells ex vivo and implanting
 treated cells, or for other conditions associated with levels of
 oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 can also be used to correlate inhibition of gene expression with
 alterations in phenotype, particularly for identification of therapeutic
 targets, and as research reagents (for RNA, in the same way that
 restriction endonucleases are used with DNA). The combination of
 modifications in (A) improves resistance to nucleases, binding affinity
 and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
 hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 their corresponding target sequences. AAA26219 to AAA26271 represent
 other ribozyme sequences and antisense oligonucleotides used in the
 exemplification of the present invention.
 Sequence 17 BP; 7 A; 2 C; 1 G; 7 T; 0 other;
 Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Y 1610 AACATTAAATAT 1623
 b |||||
 4 AACTTTTAAATAT 17
 RESULT 804
 AAA25891
 AAA25891 standard; DNA; 17 BP.
 AAA25891;
 19-JUL-2000 (first entry)
 Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2389.
 Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 gene expression modification; cancer; phosphorothioate; endonuclease;
 anticancer; breast cancer; endometrium cancer; ss.
 Homo sapiens.
 WO9954459-A2.
 28-OCT-1999.
 19-APR-1999; 99WO-US08547.
 20-APR-1998; 98US-0082404.
 23-JUN-1998; 98US-0103636.
 (RIBO-) RIBOZYME PHARM INC.
 Thompson JD, Beigelman L, McSwiggen JA, Karpetsky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 XX Matulic-Adamic J;
 DR WPI; 2000-013248/01.
 XX New nucleic acids that interact, and optionally cleave, target
 PT sequences, used to treat cancer -
 XX Claim 77; Page 94; 148pp; English.
 XX The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any
 CC catalytic nucleic acid (A') that modulates expression of the oestrogen
 CC receptor gene, are used to treat cancer (particularly of breast or
 CC endometrium), in vivo or by transforming cells ex vivo and implanting
 CC treated cells, or for other conditions associated with levels of
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 CC can also be used to correlate inhibition of gene expression with
 CC alterations in phenotype, particularly for identification of therapeutic
 CC targets, and as research reagents (for RNA, in the same way that
 CC restriction endonucleases are used with DNA). The combination of
 CC modifications in (A) improves resistance to nucleases, binding affinity
 CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 CC their corresponding target sequences. AAA26219 to AAA26271 represent
 CC other ribozyme sequences and antisense oligonucleotides used in the
 CC exemplification of the present invention.
 XX Sequence 17 BP; 7 A; 1 C; 2 G; 7 T; 0 other;
 SQ Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1610 AACATTAAATAT 1623
 Db |||||
 3 AACTTTTAAATAT 16
 RESULT 805
 AAA25892
 ID AAA25892 standard; DNA; 17 BP.
 XX AC
 AC AAA25892;
 XX
 DT 19-JUL-2000 (first entry)
 XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2390.
 DE Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX Homo sapiens.
 OS
 XX WO9954459-A2.
 PN
 XX 28-OCT-1999.
 XX
 XX 19-APR-1999; 99WO-US08547.
 PF
 XX 20-APR-1998; 98US-0082404.
 PR
 XX 23-JUN-1998; 98US-0103636.
 PR
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Thompson JD, Beigelman L, McSwiggen JA, Karpetsky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;

XX WPI; 2000-013248/01.
 XX New nucleic acids that interact, and optionally cleave, target
 XX sequences, used to treat cancer -
 XX Claim 77; Page 94; 148pp; English.
 XX The present invention describes nucleic acids (A) that interact stably
 XX with a target sequence and contain at least one phosphorodithioate
 XX link, having endonuclease activity. (A), and more generally any
 XX catalytic nucleic acid (A') that modulates expression of the oestrogen
 XX receptor gene, are used to treat cancer (particularly of breast or
 XX endometrium), in vivo or by transforming cells ex vivo and implanting
 XX treated cells, or for other conditions associated with levels of
 XX oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 XX can also be used to correlate inhibition of gene expression with
 XX alterations in phenotype, particularly for identification of therapeutic
 XX targets, and as research reagents (for RNA, in the same way that
 XX restriction endonucleases are used with DNA). The combination of
 XX modifications in (A) improves resistance to nucleases, binding affinity
 XX and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
 XX hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 XX corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 XX receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 XX their corresponding target sequences. AAA26219 to AAA26271 represent
 XX other ribozyme sequences and antisense oligonucleotides used in the
 XX exemplification of the present invention.
 XX Sequence 17 BP; 7 A; 1 C; 2 G; 7 T; 0 other;
 XX Query Match 1.0%; Score 12.4; DB 1; Length 17;
 XX Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX 1610 AACATTAAATAT 1623
 XX |||||
 XX 2 AACTTTAAATAT 15
 XX
 XX RESULT 806
 XX ID AAA25992/c
 XX AC AAA25992 standard; DNA; 17 BP.
 XX AC AAA25992;
 XX 19-JUL-2000 (first entry)
 XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2490.
 XX Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
 XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 XX gene expression modification; cancer; phosphorothioate; endonuclease;
 XX anticancer; breast cancer; endometrium cancer; ss.
 XX Homo sapiens.
 XX WO9954459-A2.
 XX 28-OCT-1999.
 XX 19-APR-1999; 99WO-US08547.
 XX 20-APR-1998; 98US-0082404.
 XX 23-JUN-1998; 98US-0103636.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Thompson JD, Beigelman L, McSwiggen JA, Karpelisky A, Bellon L;
 XX Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
 XX Matulic-Adamic J;
 XX WPI; 2000-013248/01.

XX New nucleic acids that interact, and optionally cleave, target
 XX sequences, used to treat cancer -
 XX Claim 77; Page 97; 148pp; English.
 XX The present invention describes nucleic acids (A) that interact stably
 XX with a target sequence and contain at least one phosphorodithioate
 XX link, having endonuclease activity. (A), and more generally any
 XX catalytic nucleic acid (A') that modulates expression of the oestrogen
 XX receptor gene, are used to treat cancer (particularly of breast or
 XX endometrium), in vivo or by transforming cells ex vivo and implanting
 XX treated cells, or for other conditions associated with levels of
 XX oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 XX can also be used to correlate inhibition of gene expression with
 XX alterations in phenotype, particularly for identification of therapeutic
 XX targets, and as research reagents (for RNA, in the same way that
 XX restriction endonucleases are used with DNA). The combination of
 XX modifications in (A) improves resistance to nucleases, binding affinity
 XX and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
 XX hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 XX corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 XX receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 XX their corresponding target sequences. AAA26219 to AAA26271 represent
 XX other ribozyme sequences and antisense oligonucleotides used in the
 XX exemplification of the present invention.
 XX Sequence 17 BP; 9 A; 1 C; 2 G; 5 T; 0 other;
 XX Query Match 1.0%; Score 12.4; DB 1; Length 17;
 XX Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX 599 ATTATTATTGGAA 612
 XX |||||
 XX 15 ATTCTTTATTGGAA 2
 XX
 XX RESULT 807
 XX ID ABA77737
 XX AC ABA77737 standard; DNA; 17 BP.
 XX AC ABA77737;
 XX 24-JAN-2002 (first entry)
 XX Retinoblastoma mutation correcting oligonucleotide SEQ ID NO: 583.
 XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 XX retinoblastoma; BRCA1; BRCA2; CTR; cystic fibrosis; cancer; Factor V;
 XX cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 XX adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 XX haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 XX mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 XX familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 XX UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 XX Alzheimer's disease; cytostatic; antitickling; antianaemic; haemostatic;
 XX antilipemic; ss.
 XX Homo sapiens.
 XX WO200173002-A2.
 XX 04-OCT-2001.
 XX 27-MAR-2001; 2001WO-US09761.
 XX 27-MAR-2000; 2000US-192176P.
 XX 27-MAR-2000; 2000US-192179P.
 XX 01-JUN-2000; 2000US-208538P.
 XX 30-OCT-2000; 2000US-244989P.
 XX (UYDE) UNIV DELAWARE.

X I Kmiec EB, Camper HB, Rice MC;
 X R WPI; 2001-639230/73.
 X T Oligonucleotide for targeted alterations of genetic sequences and for
 X T treating cystic fibrosis, comprises at least one mismatch and chemical
 X T modification -
 X S Claim 7; Page 79; 294pp; English.
 X C The present invention provides single-stranded oligonucleotides which can
 C be used for the targeted alteration of genomic sequences, where the
 C oligonucleotide has at least one mismatch compared with the genomic
 C sequence to be altered. In particular, these sequences are directed at
 C the following genes: adenosine deaminase, p53, beta-globin,
 C retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 C (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 C 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 C apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 C (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 C presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 C such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 C haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 C Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 C various syndromes. The present sequence is one of the gene correcting
 C oligonucleotides of the invention.
 X X Sequence 17 BP; 9 A; 2 C; 1 G; 5 T; 0 other;
 Q Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Y 1204 ATTAAACAACAA 1217
 b |||||
 3 ATTAAACAACAA 16
 RESULT 808
 BA7738/c
 D ABA77738 standard; DNA; 17 BP.
 X C ABA77738;
 X T 24-JAN-2002 (first entry)
 X Z Retinoblastoma mutation correcting oligonucleotide SEQ ID NO: 594.
 W Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 W retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 W cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 W adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 W haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 W mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 W familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 W UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 W Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
 W antileptic; ss.
 S Homo sapiens.
 X N WO200173002-A2.
 X D 04-OCT-2001.
 X F 27-MAR-2001; 2001WO-US09761.
 X R 27-MAR-2000; 2000US-192176P.
 R 27-MAR-2000; 2000US-192179P.
 R 01-JUN-2000; 2000US-208538P.
 R 30-OCT-2000; 2000US-244989P.

PA (UTDE) UNIV DELAWARE.
 XX Kmiec EB, Camper HB, Rice MC;
 PI WPI; 2001-639230/73.
 XX Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification -
 XX Claim 7; Page 79; 294pp; English.
 XX The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention.
 XX XQ Sequence 17 BP; 5 A; 1 C; 2 G; 9 T; 0 other;
 Q Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1204 ATTAAACAACAA 1217
 DB |||||
 15 ATTAAACAACAA 2
 RESULT 809
 ABA80208
 ID ABA80208 standard; DNA; 17 BP.
 XX ABA80208;
 XX 24-JAN-2002 (first entry)
 XX MLH1 mutation correcting oligonucleotide SEQ ID NO: 3054.
 XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 XX retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 XX cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 XX adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 XX haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 XX mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 XX familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 XX UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 XX Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
 XX antileptic; ss.
 XX Homo sapiens.
 OS WO200173002-A2.
 XX 04-OCT-2001.
 XX 27-MAR-2001; 2001WO-US09761.
 XX 27-MAR-2000; 2000US-192176P.
 PR 27-MAR-2000; 2000US-192179P.
 PR 01-JUN-2000; 2000US-208538P.
 PR 30-OCT-2000; 2000US-244989P.

XX (UYDE) UNIV DELAWARE.
 XX Kmiec EB, Gamper HB, Rice MC;
 XX WPI; 2001-639230/73.
 XX
 XX Oligonucleotide for targeted alterations of genetic sequences and for
 XX treating cystic fibrosis, comprises at least one mismatch and chemical
 XX modification -
 XX
 XX Claim 7; Page 213; 294pp; English.
 XX
 XX The present invention provides single-stranded oligonucleotides which can
 XX be used for the targeted alteration of genomic sequences, where the
 XX oligonucleotide has at least one mismatch compared with the genomic
 XX sequence to be altered. In particular, these sequences are directed at
 XX the following genes: adenosine deaminase, p53, beta-globin,
 XX retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 XX 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 XX apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 XX (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 XX such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 XX haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 XX Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 XX various syndromes. The present sequence is one of the gene correcting
 XX oligonucleotides of the invention.
 XX
 XX Sequence 17 BP; 6 A; 3 C; 3 G; 5 T; 0 other;
 XX
 XX Query Match 1.0%; Score 12.4; DB 1; Length 17;
 XX Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 533 TTCAGTAAACAATG 546
 XX ||||| |||||
 XX 4 TTCAGTACACAATG 17
 XX
 XX
 XX RESULT 810
 XX ABA80209/c
 XX ID ABA80209 standard; DNA; 17 BP.
 XX AC ABA80209;
 XX
 XX 24-JAN-2002 (first entry)
 XX
 XX MLH1 mutation correcting oligonucleotide SEQ ID NO: 3055.
 XX
 XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 XX retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; Cancer; Factor V;
 XX cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 XX adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 XX haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 XX mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 XX familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 XX UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 XX Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
 XX antilipemic; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200173002-A2.
 XX
 XX 04-OCT-2001.
 XX
 XX 27-MAR-2001; 2001WO-US09761.
 XX
 XX 27-MAR-2000; 2000US-192178P.
 XX
 XX 27-MAR-2000; 2000US-192179P.
 XX
 XX 01-JUN-2000; 2000US-208538P.

PR 30-OCT-2000; 2000US-244989P.
 XX (UYDE) UNIV DELAWARE.
 XX Kmiec EB, Gamper HB, Rice MC;
 XX WPI; 2001-639230/73.
 XX
 XX Oligonucleotide for targeted alterations of genetic sequences and for
 XX treating cystic fibrosis, comprises at least one mismatch and chemical
 XX modification -
 XX
 XX Claim 7; Page 213; 294pp; English.
 XX
 XX The present invention provides single-stranded oligonucleotides which can
 XX be used for the targeted alteration of genomic sequences, where the
 XX oligonucleotide has at least one mismatch compared with the genomic
 XX sequence to be altered. In particular, these sequences are directed at
 XX the following genes: adenosine deaminase, p53, beta-globin,
 XX retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 XX 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 XX apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 XX (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 XX such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 XX haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 XX Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 XX various syndromes. The present sequence is one of the gene correcting
 XX oligonucleotides of the invention.
 XX
 XX Sequence 17 BP; 5 A; 3 C; 3 G; 6 T; 0 other;
 XX
 XX Query Match 1.0%; Score 12.4; DB 1; Length 17;
 XX Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 533 TTCAGTAAACAATG 546
 XX ||||| |||||
 XX 14 TTCAGTACACAATG 1
 XX
 XX
 XX RESULT 811
 XX AAH74941
 XX ID AAH74941 standard; DNA; 17 BP.
 XX AC AAH74941;
 XX
 XX 29-OCT-2001 (first entry)
 XX
 XX Nucleotide sequence identified using ligation-based DNA sequencing.
 XX
 XX Nucleotide sequence signature; nucleotide sequencing; ss.
 XX
 XX Unidentified.
 XX
 XX WO200161044-A1.
 XX
 XX 23-AUG-2001.
 XX
 XX 15-FEB-2001; 2001WO-US05032.
 XX
 XX 15-FEB-2000; 2000US-0182454.
 XX
 XX 01-SEP-2000; 2000US-0654187.
 XX
 XX (LYNX-) LYNX THERAPEUTICS INC.
 XX
 XX Corcoran KC, Elétr S;
 XX
 XX WPI; 2001-522608/57.
 XX
 XX Determining nucleotide sequence signature, by obtaining optical values
 XX for each nucleotide position in a group, adjusting them to get ratio of

PT final highest values near predetermined factor, generating base call
 XX Disclosure: Fig 120; 73pp; English.
 XX The specification describes a method for determining a nucleotide
 CC sequence signature. The method comprises obtaining optical measurements
 CC with values indicating each nucleotide in a group of nucleotide
 CC positions, adjusting the values until the ratio of highest value in
 CC the set to next highest values in the set is at least a predetermined
 CC factor, and generating a base call for a position in the group based
 CC on results after the adjustment of values. The method is used for
 CC determining a signature of a nucleotide sequence, and for determining
 CC a nucleotide sequence of a polynucleotide from a series of optical
 CC measurements. AAH74913-50 represent yeast sequences, identified using
 CC the method of the invention.
 XX Sequence 17 BP; 5 A; 2 C; 2 G; 8 T; 0 other;
 SQ Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Y 1149 TTAATTAGATATT 1162
 b 3 TCAATTAGATATT 16
 RESULT 812
 AAH91169
 D AAH91169 standard; DNA; 17 BP.
 X X
 C AAH91169;
 X X
 T 09-OCT-2001 (first entry)
 X X
 E Human inflammatory bowel disease associated polymorphic site #244.
 X X
 W Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 W single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
 X chromosome 5q31-33; forensic test; gene therapy; ds.
 X Homo sapiens.
 X X
 S Key Location/Qualifiers
 H misc_feature 11
 T /tag= a
 F /note= "SNP, optionally A or T at this position"
 F WO200142511-A2.
 14-JUN-2001.
 11-DEC-2000; 2000WO-US33632.
 10-DEC-1999; 99US-0170257.
 10-APR-2000; 2000US-0196046.
 (WHD) WHITEHEAD INST BIOMEDICAL RES.
 (ELLI) ELLIPSIS BIOTHERAPEUTICS CORP.
 Daly M, Hudson TJ, Lander BS, Rioux J, Siminovitch K;
 WPI; 2001-367874/38.
 Testing for the presence of polymorphisms associated with inflammatory
 bowel disease, using a hybridization assay -
 Claim 1; Page 49; 463pp; English.
 The present invention describes a method for detecting the presence of
 polymorphisms associated with inflammatory bowel diseases such as
 ulcerative colitis and Crohn's disease. The methods can be used to detect
 the presence of genetic polymorphisms associated with inflammatory bowel

CC disease and correlating their occurrence with disease states. They may be
 CC used in this way for phenotypic correlations, forensics, paternity
 CC testing, medicine and genetic analysis. The present sequence is a
 CC polymorphic site described in the exemplification of the invention.
 XX Sequence 17 BP; 3 A; 4 C; 1 G; 8 T; 1 other;
 SQ Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Y 1555 TCCTCAAAATTTT 1569
 b 3 TCCTCAACATTTT 17
 RESULT 813
 AAH94872
 ID AAH94872 standard; RNA; 17 BP.
 X X
 AC AAH94872;
 X X
 DT 09-OCT-2001 (first entry)
 X X
 DE Human Chk1 ribozyme substrate SEQ ID NO: 297.
 X X
 KW Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
 KW RNA cleavage; cancer; ss.
 X X
 OS Homo sapiens.
 X X
 FN WO200157206-A2.
 X X
 PD 09-AUG-2001.
 X X
 PF 02-FEB-2001; 2001WO-US03504.
 X X
 PR 03-FEB-2000; 2000US-0179983.
 X X
 PA (RIBO-) RIBOZYME PHARM INC.
 X X
 PI (FATT/) FATTAEY A R.
 X X
 PI Fattaeay AR, Jarvis T, McSwiggen J, Booher RN, Holman PS;
 X X
 DR WPI; 2001-496922/54.
 X X
 PT Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
 PT molecules, which downregulates expression of a checkpoint kinase-1
 PT gene, useful for treating colorectal, lung, breast or prostate cancers
 X X
 PS Claim 4; Page 58; 115pp; English.
 X X
 CC The present invention provides nucleic acid molecules capable of
 CC downregulating the expression of the human checkpoint kinase-1 (Chk1)
 CC gene. These may be antisense or ribozyme sequences, and are useful in the
 CC treatment of diseases associated with conditions affected by Chk1 levels,
 CC including cancer. The present sequence is an oligonucleotide described in
 CC the exemplification of the invention.
 X X
 SQ Sequence 17 BP; 3 A; 2 C; 1 G; 11 U; 0 other;
 SQ Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 21.4%; Pred. No. 5.1e+02;
 Matches 3; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
 Y 1141 AATTATTATTATT 1154
 b 4 AAUUAUUUUUUU 17
 RESULT 814
 AAH94873

D AAH94873 standard; RNA; 17 BP.
 X
 C AAH94873;
 X
 T 09-OCT-2001 (first entry)
 X
 E Human Chk1 ribozyme substrate SEQ ID NO: 298.
 X
 X Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
 M RNA cleavage; cancer; ss.
 X
 S Homo sapiens.
 X
 N WO200157206-A2.
 N
 D 09-AUG-2001.
 X
 X 02-FEB-2001; 2001WO-US03504.
 P
 R 03-FEB-2000; 2000US-0179983.
 X
 X (RIBO-) RIBOZYME PHARM INC.
 A (FATT/) FATTAEY A R.
 A
 Fattaey AR, Jarvis T, McSwiggen J, Booher RN, Holman PS;
 WPI; 2001-496922/54.
 X
 X Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
 X molecules, which downregulates expression of a checkpoint kinase-1
 X gene, useful for treating colorectal, lung, breast or prostate cancers
 X
 X Claim 4; Page 58; 115pp; English.
 X
 X The present invention provides nucleic acid molecules capable of
 X downregulating the expression of the human checkpoint kinase-1 (Chk1)
 X gene. These may be antisense or ribozyme sequences, and are useful in the
 X treatment of diseases associated with conditions affected by Chk1 levels,
 X including cancer. The present sequence is an oligonucleotide described in
 X the exemplification of the invention.
 X
 X Sequence 17 BP; 3 A; 1 C; 2 G; 11 U; 0 other;
 S
 X Query Match 1.0%; Score 12.4; DB 1; Length 17;
 X Best Local Similarity 21.4%; Pred. No. 5.1e+02;
 X Matches 3; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
 X
 QY 1141 AATTATTTTATTT 1154
 D 2 AAUUAUUUUUUU 15
 D
 RESULT 815
 AAH94874
 ID AAH94874 standard; RNA; 17 BP.
 X
 X AAH94874;
 A
 X 09-OCT-2001 (first entry)
 X
 X Human Chk1 ribozyme substrate SEQ ID NO: 299.
 DE Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
 X RNA cleavage; cancer; ss.
 X
 X Homo sapiens.
 OS
 X WO200157206-A2.
 X
 X 09-AUG-2001.
 PD
 X 02-FEB-2001; 2001WO-US03504.
 PF

XX 03-FEB-2000; 2000US-0179983.
 PR (RIBO-) RIBOZYME PHARM INC.
 XX (FATT/) FATTAEY A R.
 PA
 XX Fattaey AR, Jarvis T, McSwiggen J, Booher RN, Holman PS;
 PI WPI; 2001-496922/54.
 XX
 DR Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
 XX molecules, which downregulates expression of a checkpoint kinase-1
 PT gene, useful for treating colorectal, lung, breast or prostate cancers
 PT
 PT
 X Claim 4; Page 58; 115pp; English.
 XX
 XX The present invention provides nucleic acid molecules capable of
 CC downregulating the expression of the human checkpoint kinase-1 (Chk1)
 CC gene. These may be antisense or ribozyme sequences, and are useful in the
 CC treatment of diseases associated with conditions affected by Chk1 levels,
 CC including cancer. The present sequence is an oligonucleotide described in
 CC the exemplification of the invention.
 X
 X Sequence 17 BP; 3 A; 0 C; 2 G; 12 U; 0 other;
 S
 X Query Match 1.0%; Score 12.4; DB 1; Length 17;
 X Best Local Similarity 21.4%; Pred. No. 5.1e+02;
 X Matches 3; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
 X
 QY 1141 AATTATTTTATTT 1154
 D 1 AAUUAUUUUUUU 14
 D
 RESULT 816
 AAH95728
 ID AAH95728 standard; RNA; 17 BP.
 X
 X AAH95728;
 AC
 X 09-OCT-2001 (first entry)
 DT
 X Human Chk1 ribozyme substrate SEQ ID NO: 1153.
 DE Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
 X RNA cleavage; cancer; ss.
 X
 X Homo sapiens.
 OS
 X WO200157206-A2.
 X
 X 09-AUG-2001.
 PD
 X 02-FEB-2001; 2001WO-US03504.
 PF
 X 03-FEB-2000; 2000US-0179983.
 PR
 X (RIBO-) RIBOZYME PHARM INC.
 PA (FATT/) FATTAEY A R.
 X
 X Fattaey AR, Jarvis T, McSwiggen J, Booher RN, Holman PS;
 PI WPI; 2001-496922/54.
 XX
 XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
 X molecules, which downregulates expression of a checkpoint kinase-1
 PT gene, useful for treating colorectal, lung, breast or prostate cancers
 PT
 PT
 X Claim 4; Page 81; 115pp; English.
 XX
 XX The present invention provides nucleic acid molecules capable of

downregulating the expression of the human checkpoint kinase-1 (Chk1) gene. These may be antisense or ribozyme sequences, and are useful in the treatment of diseases associated with conditions affected by Chk1 levels, including cancer. The present sequence is an oligonucleotide described in the exemplification of the invention.

Sequence 17 BP; 3 A; 2 C; 1 G; 11 U; 0 other;
Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 21.4%; Pred. No. 5.1e+02;
Matches 3; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

1141 AATTATTATTATT 1154
|||||:||||: |||
4 AAUUAUUUUUUU 17

RESULT 817
AF26858
J AAF26858 standard; DNA; 17 BP.

AAF26858;

09-APR-2001 (first entry)

SR alpha sequence SV40 promoter sequence SEQ ID NO:1.

Simian virus 40; SV40; SR-alpha; promoter; regulatory sequence; expression vector; ds.

Rhesus macaque polyoma virus.

WO200077231-A1.

21-DEC-2000.

16-JUN-2000; 2000WO-JP03956.

16-JUN-1999; 99JP-0170355.

(MEIP) MEIJI MILK PROD CO LTD.

(REIN-) RES INST INNOVATIVE TECHNOLOGY EARTH.

Nakanichi N, Hirota Y, Ito M, Maeda T, Yan H, Matsumura T;

WPI; 2001-112226/12.

Regulatory sequences for constructing recombinant expression vector for animal cells, with expression efficiency to produce eg. protein drugs in high yield with selectivity safety and rapidity but without self-replication

Claim 4; Page 23; 80pp; Japanese.

The present invention describes a DNA (I) comprising an SR-alpha promoter enhancer sequence (SRalpha sequence) constructed from an SV40-originated replication starting point, an enhancer sequence and an initiation promoter sequence. (I) further comprises an HTLV-1 originated LTR-A sequence and a part of the U5 sequence (U' sequence), with the ligation of a post-transcriptional regulatory sequence (SRalphaSP sequence) through an SV40 late stage mRNA splice signal sequence (Sp sequence) to the 3'-downstream in which an ATG sequence is modified by GCA sequence in the Sp sequence in the transcription to give the post-transcription regulatory sequence. Such produced animal cells have expression efficiency, including transcription and translation, to produce e.g. protein drugs in high yield with selectivity safety and rapidity but without self-replication in presence of T antigen. The regulatory sequences are for constructing recombinant expression vector for use with animal cells. Such produced animal cells have expression efficiency, including transcription and translation, to produce e.g. protein drugs in high yield with selectivity safety and rapidity but without self-replication in presence of T antigen. The present sequence represents an SR-alpha sequence SV40 promoter sequence which is given

CC in the exemplification of the present invention.

XX Sequence 17 BP; 4 A; 0 C; 0 G; 13 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1141 AATTATTATTATT 1154

|||||:||||: |||
2 AATTATTATTATT 15

RESULT 818

ABK00458/C

ID ABK00458 standard; RNA; 17 BP.

XX ABK00458;

DT 12-MAR-2002 (first entry)

Human NOGO Hammerhead Ribozyme #458.

Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNzyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; INC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

PD 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US04273.

XX 11-FEB-2000; 2000US-181797P.

XX 28-FEB-2000; 2000US-185516P.

XX 08-MAR-2000; 2000US-187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX Blatt L, McSwiggen J, Chowrira BM;

PI WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury

XX Claim 88; Page 73; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NIN motif) or an amberyne (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used

to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopenia, and inflammatory arthropathy. The NOGO-targeting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is a hammerhead ribozyme of the invention.

Sequence 17 BP; 5 A; 2 C; 1 G; 9 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1096 TAGAAGATGAATCA 1109
|||||
14 TAGAAGATGAATCA 1

RESULT 819
ABK01127
D ABK01127 standard; RNA; 17 BP.
C ABK01127;
X 12-MAR-2002 (first entry)
X Human NOGO Inozyme #397.
X Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; neurotropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

Homo sapiens.
Synthetic.
WO200159103-A2.
16-AUG-2001.
09-FEB-2001; 2001WO-US04273.
11-FEB-2000; 2000US-181797P.
28-FEB-2000; 2000US-185516P.
06-MAR-2000; 2000US-187128P.
(RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
XX (CHOW/) CHOWRIRA B M.
PI Blatt L, McSwiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury
XX Claim 88; Page 84; 200pp; English.
XX The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO).
XX The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopenia, and inflammatory arthropathy. The NOGO-targeting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an inozyme of the invention.

Sequence 17 BP; 7 A; 3 C; 2 G; 5 U; 0 other;
Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 5.1e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 623 ACAACAAATATTT 636
|||||
Db 4 ACAACAGAAUAUU 17

RESULT 820
ABK02182
ID ABK02182 standard; RNA; 17 BP.
XX AC ABK02182;
XX 12-MAR-2002 (first entry)
XX Human NOGO DNazyme #94.
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; neurotropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;

Dr. J. H. B. Smith

CC associated

CC associated

use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus), associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an amberzyme molecule of the invention.

Sequence 17 BP; 8 A; 3 C; 1 G; 5 U; 0 other;

Query Match 1.08; Score 12.4; DB 1; Length 17;
 Best Local Similarity 64.38; Pred. No. 5.1e+02;
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

623 ACAACAAATATTT 636
 ||||| :|||:
 3 ACAACAGAAUAUU 16

RESULT 822
 ABK02556
 ID ABK02556 standard; RNA; 17 BP.
 KC ABK02556;
 XT 12-MAR-2002 (first entry)
 JE Human NOGO Amberzyme #228.

Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; neurotropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNzyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; neurodegenerative disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

Homo sapiens.
 Synthetic.
 WO200159103-A2.
 16-AUG-2001.
 09-FEB-2001; 2001WO-US04273.
 11-FEB-2000; 2000US-181797P.
 28-FEB-2000; 2000US-185516P.
 06-MAR-2000; 2000US-187128P.
 (RIBO-) RIBOZYME PHARM INC.
 (BLAT/) BLATT L.
 (MCSW/) MCSWIGGEN J.
 (CHOW/) CHOWRIRA B M.

Blatt L, McSwiggen J, Chowrira BM;
 WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury -

Claim 88; Page 135; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA with a XGY motif). The CD20-targeting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus), associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an amberzyme molecule of the invention.

Sequence 17 BP; 11 A; 1 C; 2 G; 3 U; 0 other;

Query Match 1.08; Score 12.4; DB 1; Length 17;
 Best Local Similarity 78.68; Pred. No. 5.1e+02;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1204 ATTTAAACAAACAAA 1217
 :|||:|||||
 3 AUAAGAAGAAACAAA 16

RESULT 823
 ABEV80423/c
 ID ABEV80423 standard; DNA; 17 BP.
 KC ABEV80423;
 XT 03-JAN-2003 (first entry)
 JE Human HTPL scanning oligonucleotide SEQ ID 1569.

Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
 Homo sapiens.
 EP1229046-A2.

K 07-AUG-2002.
 K 28-JAN-2002; 2002EP-0001167.
 K 30-JAN-2001; 2001WO-US00663.
 K 30-JAN-2001; 2001WO-US00664.
 K 30-JAN-2001; 2001WO-US00665.
 K 30-JAN-2001; 2001WO-US00667.
 K 30-JAN-2001; 2001WO-US00668.
 K 23-MAY-2001; 2001US-0864761.
 K 09-OCT-2001; 2001US-0327898.
 K (AEOM-) AEOMICA INC.
 K Zhan J;
 K WPI; 2002-676582/73.
 K Novel isolated human testis expressed Patched like protein (HTPL),
 K useful for identifying agonist and antagonist and specific binding
 K partners, and for treating subjects having defects in HTPL -
 K Example 2; Page 282; 718pp; English.
 K The present invention relates to human testis expressed Patched like
 K protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
 K has two isoforms, with a few single base pair differences between the
 K two. One of the single base pair changes introduces a premature stop
 K codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 K shares an overall structure organisation with the Patched protein. The
 K shared structural features strongly imply that HTPL plays a role similar
 K to that of Patched, and is a potential tumour suppressor. HTPL is
 K important in regulating male germ cell development, and the HTPL gene was
 K mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 K useful for diagnosing a disorder caused by mutation in HTPL, and in
 K therapy and manufacture of a medicament for treatment or prevention of
 K such disorder associated with decreased expression or activity of human
 K HTPL. Such disorders include disorders of testis, or adrenal, adult and
 K foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 K skeletal muscle or colon function. HTPL proteins and nucleic acids are
 K clinically useful diagnostic markers and potential therapeutic agents for
 K male infertility and cancer. The present oligonucleotide was used in an
 K example from the invention.
 K Sequence 17 BP; 2 A; 1 C; 2 G; 12 T; 0 other;
 K Query Match 1.0%; Score 12.4; DB 1; Length 17;
 K Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 K Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Y 678 ACAATAGCAAAAT 691
 b 17 AAAATAGCAAAAT 4
 RESULT 824
 BV80429/c
 D ABV80429 standard; DNA; 17 BP.
 X ABV80429;
 X 03-JAN-2003 (first entry)
 X Human HTPL scanning oligonucleotide SEQ ID 1675.
 X Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 X human testis expressed Patched like protein; testis; adrenal; liver;
 X male germ cell development; bone marrow; brain; kidney; lung; placenta;
 X prostate; skeletal muscle; colon; male infertility; cancer; ss.
 X Homo sapiens.

XX EF1229046-A2.
 XX 07-AUG-2002.
 XX 28-JAN-2002; 2002EP-0001167.
 XX 30-JAN-2001; 2001WO-US00663.
 XX 30-JAN-2001; 2001WO-US00664.
 XX 30-JAN-2001; 2001WO-US00665.
 XX 30-JAN-2001; 2001WO-US00667.
 XX 30-JAN-2001; 2001WO-US00668.
 XX 23-MAY-2001; 2001US-0864761.
 XX 09-OCT-2001; 2001US-0327898.
 XX (AEOM-) AEOMICA INC.
 XX Zhan J;
 XX WPI; 2002-676582/73.
 XX Novel isolated human testis expressed Patched like protein (HTPL),
 XX useful for identifying agonist and antagonist and specific binding
 XX partners, and for treating subjects having defects in HTPL -
 XX Example 2; Page 283; 718pp; English.
 XX The present invention relates to human testis expressed Patched like
 XX protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
 XX has two isoforms, with a few single base pair differences between the
 XX two. One of the single base pair changes introduces a premature stop
 XX codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 XX shares an overall structure organisation with the Patched protein. The
 XX shared structural features strongly imply that HTPL plays a role similar
 XX to that of Patched, and is a potential tumour suppressor. HTPL is
 XX important in regulating male germ cell development, and the HTPL gene was
 XX mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 XX useful for diagnosing a disorder caused by mutation in HTPL, and in
 XX therapy and manufacture of a medicament for treatment or prevention of
 XX such disorder associated with decreased expression or activity of human
 XX HTPL. Such disorders include disorders of testis, or adrenal, adult and
 XX foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 XX skeletal muscle or colon function. HTPL proteins and nucleic acids are
 XX clinically useful diagnostic markers and potential therapeutic agents for
 XX male infertility and cancer. The present oligonucleotide was used in an
 XX example from the invention.
 XX Sequence 17 BP; 5 A; 2 C; 1 G; 9 T; 0 other;
 XX Query Match 1.0%; Score 12.4; DB 1; Length 17;
 XX Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 675 TATACAAATAGCAA 688
 Db 14 TATACAAATAGCAA 1
 RESULT 825
 ABV80681/c
 ID ABV80681 standard; DNA; 17 BP.
 XX ABV80681;
 XX 03-JAN-2003 (first entry)
 XX Human HTPL scanning oligonucleotide SEQ ID 1927.
 XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 XX human testis expressed Patched like protein; testis; adrenal; liver;
 XX male germ cell development; bone marrow; brain; kidney; lung; placenta;
 XX prostate; skeletal muscle; colon; male infertility; cancer; ss.

X S Homo sapiens.
X N EP1229046-A2.
X D 07-AUG-2002.
X F 28-JAN-2002; 2002EP-0001167.
X R 30-JAN-2001; 2001WO-US00563.
X R 30-JAN-2001; 2001WO-US00564.
X R 30-JAN-2001; 2001WO-US00565.
X R 30-JAN-2001; 2001WO-US00567.
X R 30-JAN-2001; 2001WO-US00568.
X R 30-JAN-2001; 2001WO-US00569.
X R 23-MAY-2001; 2001US-0864761.
X R 09-OCT-2001; 2001US-0327898.
X A (AEOM-) AEOMICA INC.
X I Zhan J;
X I WPI; 2002-676582/73.
X R Novel isolated human testis expressed Patched like protein (HTPL),
X T useful for identifying agonist and antagonist and specific binding
X T partners, and for treating subjects having defects in HTPL -
X S Example 2; Page 316; 718pp; English.
X C The present invention relates to human testis expressed Patched like
X C protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
X C has two isoforms, with a few single base pair differences between the
X C two. One of the single base pair changes introduces a premature stop
X C codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
X C shares an overall structure organisation with the Patched protein. The
X C shared structural features strongly imply that HTPL plays a role similar
X C to that of Patched, and is a potential tumour suppressor. HTPL is
X C important in regulating male germ cell development, and the HTPL gene was
X C mapped to human chromosome 10p12.1. HTPL and its coding sequence are
X C useful for diagnosing a disorder caused by mutation in HTPL, and in
X C therapy and manufacture of a medicament for treatment or prevention of
X C such disorder associated with decreased expression or activity of human
X C HTPL. Such disorders include disorders of testis, or adrenal, adult and
X C foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
X C skeletal muscle or colon function. HTPL proteins and nucleic acids are
X C clinically useful diagnostic markers and potential therapeutic agents for
X C male infertility and cancer. The present oligonucleotide was used in an
X C example from the invention.
X C Sequence 17 BP; 5 A; 2 C; 2 G; 8 T; 0 other;
X C Query Match 1.0%; Score 12.4; DB 1; Length 17;
X C Best Local Similarity 92.9%; Pred. No. 5.1e+02;
X C Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 1459 TTATTATGTACAA 1472
X 17 TTATGATGTACAA 4
RESULT 826
ID ABV80682/c
X AC ABV80682 standard; DNA; 17 BP.
X AC ABV80682;
X DT 03-JAN-2003 (first entry)
X DE Human HTPL scanning oligonucleotide SEQ ID 1928.
X CW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
X CW human testis expressed Patched like protein; testis; adrenal; liver;

XW male germ cell development; bone marrow; brain; kidney; lung; placenta;
XW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX Homo sapiens.
XX EP1229046-A2.
XX 07-AUG-2002.
XX 28-JAN-2002; 2002EP-0001167.
XX 30-JAN-2001; 2001WO-US00663.
XX 30-JAN-2001; 2001WO-US00664.
XX 30-JAN-2001; 2001WO-US00665.
XX 30-JAN-2001; 2001WO-US00667.
XX 30-JAN-2001; 2001WO-US00668.
XX 30-JAN-2001; 2001WO-US00669.
XX 23-MAY-2001; 2001US-0864761.
XX 09-OCT-2001; 2001US-0327898.
XX (AEOM-) AEOMICA INC.
XX Zhan J;
XX WPI; 2002-676582/73.
XX Novel isolated human testis expressed Patched like protein (HTPL),
XX useful for identifying agonist and antagonist and specific binding
XX partners, and for treating subjects having defects in HTPL -
XX Example 2; Page 316; 718pp; English.
XX The present invention relates to human testis expressed Patched like
XX protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
XX has two isoforms, with a few single base pair differences between the
XX two. One of the single base pair changes introduces a premature stop
XX codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
XX shares an overall structure organisation with the Patched protein. The
XX shared structural features strongly imply that HTPL plays a role similar
XX to that of Patched, and is a potential tumour suppressor. HTPL is
XX important in regulating male germ cell development, and the HTPL gene was
XX mapped to human chromosome 10p12.1. HTPL and its coding sequence are
XX useful for diagnosing a disorder caused by mutation in HTPL, and in
XX therapy and manufacture of a medicament for treatment or prevention of
XX such disorder associated with decreased expression or activity of human
XX HTPL. Such disorders include disorders of testis, or adrenal, adult and
XX foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
XX skeletal muscle or colon function. HTPL proteins and nucleic acids are
XX clinically useful diagnostic markers and potential therapeutic agents for
XX male infertility and cancer. The present oligonucleotide was used in an
XX example from the invention.
XX Sequence 17 BP; 5 A; 2 C; 3 G; 7 T; 0 other;
XX Query Match 1.0%; Score 12.4; DB 1; Length 17;
XX Best Local Similarity 92.9%; Pred. No. 5.1e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1459 TTATTATGTACAA 1472
X 16 TTATGATGTACAA 3
Db
RESULT 827
ID ABV74670
X AC ABV74670 standard; DNA; 17 BP.
X AC ABV74670;
X DT 24-DEC-2002 (first entry)
X DE Human PAPP-Ba associated 17-mer SEQ ID 196.
X CW

PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.

Homo sapiens.

US2002102252-A1.

01-AUG-2002.

06-APR-2001; 2001US-0827998.

26-MAY-2000; 2000US-207456P.

(GUY/) GU Y.

(SHAN/) SHANNON M E.

Gu Y, Shannon ME;

WPI; 2002-697817/75.

New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy - Example 2; Page 101; 353pp; English.

This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, hPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.

Sequence 17 BP; 6 A; 1 C; 1 G; 9 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 5.1e-02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1501 TGCATTTTAAATA 1514

||||| |||||

4 TGCATTTTAAATA 17

RESULT 828

BS74671

D ABS74671 standard; DNA; 17 BP.

C ABS74671;

24-DEC-2002 (first entry)

Human PAPP-Ea associated 17-mer SEQ ID 197.

PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.

Homo sapiens.

US2002102252-A1.

01-AUG-2002.

06-APR-2001; 2001US-0827998.

PR 26-MAY-2000; 2000US-207456P.

XX (GUY/) GU Y.

PA (SHAN/) SHANNON M E.

XX Gu Y, Shannon ME;

XX WPI; 2002-697817/75.

XX New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy - Example 2; Page 101; 353pp; English.

XX This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, hPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.

XX Sequence 17 BP; 7 A; 1 C; 1 G; 8 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 5.1e-02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1501 TGCATTTTAAATA 1514

||||| |||||

3 TGCATTTTAAATA 16

RESULT 829

ABS74672

ID ABS74672 standard; DNA; 17 BP.

XX ABS74672;

24-DEC-2002 (first entry)

Human PAPP-Ea associated 17-mer SEQ ID 198.

PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.

Homo sapiens.

US2002102252-A1.

01-AUG-2002.

06-APR-2001; 2001US-0827998.

26-MAY-2000; 2000US-207456P.

(GUY/) GU Y.

(SHAN/) SHANNON M E.

Gu Y, Shannon ME;

WPI; 2002-697817/75.

New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy -

Example 2; Page 101; 353pp; English.

This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, hPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.

Sequence 17 BP; 7 A; 1 C; 2 G; 7 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1501 TGCATTTTAAATA 1514
|||||
2 TGCATTTTAAATA 15

RESULT 830

ABL60107/C
ID ABL60107 standard; DNA; 17 BP.

XX ABL60107;

AC ABL60107;

DT 16-AUG-2002 (first entry)

XX Example wild type DNA sequence probe #4 for biological array.

DE Biochip; array; probe; ss.

XX Unidentified.

OS WO200180155-A2.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-US12750.

XX 18-APR-2000; 2000US-198045P.

XX 22-NOV-2000; 2000US-252880P.

XX (COMB-) COMBIMATRIX CORP.

XX Anderson BP, Quarles PA, Ghazvini S;

XX WPI; 2002-017664/02.

XX Automated process for custom-designed biochip design, comprises obtaining desired target sequences from customer, creating sequence content motif for an array and applying the motif to a surface suitable for later detection

XX Example 10; Page 30; 47pp; English.

XX The invention relates to a novel process for a manufacturer to obtain customer orders for custom-designed biochips in an automated process. The invention also includes an automated system and process for providing a fully automated process for the design, manufacture and analysis of data for biological array devices. The sequence represents an example of a probe for a wild type sequence that may be used in a biological array of the invention.

XX Sequence 17 BP; 8 A; 1 C; 2 G; 6 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

601 TATTATTGAATC 614
|||||
16 TATTATTGAATC 3

RESULT 832

ABK56190
ID ABK56190 standard; RNA; 17 BP.

CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention.

XX Sequence 17 BP; 8 A; 1 C; 2 G; 6 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1501 TGCATTTTAAATA 1514
|||||
1 TGCATTTTAAATA 14

Db 1 TGCATTTTAAATA 14

RESULT 831

ABL60107/C
ID ABL60107 standard; DNA; 17 BP.

XX ABL60107;

AC ABL60107;

DT 16-AUG-2002 (first entry)

XX Example wild type DNA sequence probe #4 for biological array.

DE Biochip; array; probe; ss.

XX Unidentified.

XX WO200180155-A2.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-US12750.

XX 18-APR-2000; 2000US-198045P.

XX 22-NOV-2000; 2000US-252880P.

XX (COMB-) COMBIMATRIX CORP.

XX Anderson BP, Quarles PA, Ghazvini S;

XX WPI; 2002-017664/02.

XX Automated process for custom-designed biochip design, comprises obtaining desired target sequences from customer, creating sequence content motif for an array and applying the motif to a surface suitable for later detection

XX Example 10; Page 30; 47pp; English.

XX The invention relates to a novel process for a manufacturer to obtain customer orders for custom-designed biochips in an automated process. The invention also includes an automated system and process for providing a fully automated process for the design, manufacture and analysis of data for biological array devices. The sequence represents an example of a probe for a wild type sequence that may be used in a biological array of the invention.

XX Sequence 17 BP; 8 A; 1 C; 2 G; 6 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

601 TATTATTGAATC 614
|||||
16 TATTATTGAATC 3

RESULT 832

ABK56190
ID ABK56190 standard; RNA; 17 BP.

This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, hPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform

ABK56190;
 02-JUL-2002 (first entry)
 Human CLCA1 gene enzymatic nucleic acid #561.
 Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 acetylcysteine.
 Homo sapiens.
 WO200211674-A2.
 14-FEB-2002.
 09-AUG-2001; 2001WO-US24970.
 09-AUG-2000; 2000US-224383P.
 (RIBO-) RIBOZYME PHARM INC.
 (SYNT) SYNTEX USA LLC.
 (THOM) THOMPSON J.
 Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
 Grupe A;
 WPI; 2002-217145/27.
 Enzymatic polynucleotide that down regulates expression of chloride
 channel calcium activated gene, useful for treating Chronic obstructive
 pulmonary disease (COPD), chronic bronchitis and asthma -
 Claim 4; Page 63; 152pp; English.
 The invention relates to enzymatic nucleic acid molecules that down
 regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 by cleaving RNA derived from the genes. The nucleic acid sequences are
 useful as pharmaceutical agents for treating conditions such as chronic
 obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 fibrosis, obstructive bowel syndrome and any other diseases or conditions
 that are related to or will respond to the levels of CLCA1 in a cell or
 tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 hence, are useful for treatment of a patient having a condition
 associated with the level of CLCA1, where the invention further comprises
 the use of one or more therapies under conditions suitable for the
 treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 nucleic acids of the invention are also used as diagnostic tools to
 examine genetic drift and mutations within diseased cells or to detect
 the presence of CLCA1 RNA in a cell. This sequence represents an
 enzymatic nucleic acid molecule of the invention.
 Sequence 17 BP; 7 A; 1 C; 1 G; 8 U; 0 other;
 Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 42.9%; Pred. No. 5.1e+02;
 Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
 1134 TATAGTAAATTTAT 1147
 :|||:|:|:|:
 3 UAUAGUACAUUUU 16

SULT 833
 K56834
 ABK56834 standard; RNA; 17 BP.
 ABK56834;

DT 02-JUL-2002 (first entry)
 XX Human CLCA1 gene enzymatic nucleic acid #1205.
 DE Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.
 XX Homo sapiens.
 XX WO200211674-A2.
 XX 14-FEB-2002.
 XX 09-AUG-2001; 2001WO-US24970.
 PF 09-AUG-2000; 2000US-224383P.
 PR (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTEX USA LLC.
 PA (THOM) THOMPSON J.
 XX Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;
 PI WPI; 2002-217145/27.
 DR Enzymatic polynucleotide that down regulates expression of chloride
 XX channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma -
 PT Claim 4; Page 82; 152pp; English.
 PS The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention.
 XX Sequence 17 BP; 6 A; 2 C; 1 G; 8 U; 0 other;
 SQ Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 42.9%; Pred. No. 5.1e+02;
 Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
 QY 1134 TATAGTAAATTTAT 1147
 :|||:|:|:|:
 Db 1 UAUAGUACAUUUU 14
 RESULT 834
 AAD31941
 ID AAD31941 standard; DNA; 17 BP.
 XX AAD31941;
 AC AAD31941;
 XX 18-JUN-2002 (first entry)
 DT Plasmodium falciparum beta-globin gene fragment.
 XX DE

XX OS

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels

Sequence	Matches	Conservative	Mismatches	Indels	Gaps
Sequence 1	13	0	1	0	0
Sequence 2	13	0	1	0	0
Sequence 3	13	0	1	0	0
Sequence 4	13	0	1	0	0
Sequence 5	13	0	1	0	0
Sequence 6	13	0	1	0	0
Sequence 7	13	0	1	0	0
Sequence 8	13	0	1	0	0
Sequence 9	13	0	1	0	0
Sequence 10	13	0	1	0	0
Sequence 11	13	0	1	0	0
Sequence 12	13	0	1	0	0
Sequence 13	13	0	1	0	0
Sequence 14	13	0	1	0	0
Sequence 15	13	0	1	0	0
Sequence 16	13	0	1	0	0
Sequence 17	13	0	1	0	0
Sequence 18	13	0	1	0	0
Sequence 19	13	0	1	0	0
Sequence 20	13	0	1	0	0
Sequence 21	13	0	1	0	0
Sequence 22	13	0	1	0	0
Sequence 23	13	0	1	0	0
Sequence 24	13	0	1	0	0
Sequence 25	13	0	1	0	0
Sequence 26	13	0	1	0	0
Sequence 27	13	0	1	0	0
Sequence 28	13	0	1	0	0
Sequence 29	13	0	1	0	0
Sequence 30	13	0	1	0	0
Sequence 31	13	0	1	0	0
Sequence 32	13	0	1	0	0
Sequence 33	13	0	1	0	0
Sequence 34	13	0	1	0	0
Sequence 35	13	0	1	0	0
Sequence 36	13	0	1	0	0
Sequence 37	13	0	1	0	0
Sequence 38	13	0	1	0	0
Sequence 39	13	0	1	0	0
Sequence 40	13	0	1	0	0
Sequence 41	13	0	1	0	0
Sequence 42	13	0	1	0	0
Sequence 43	13	0	1	0	0
Sequence 44	13	0	1	0	0
Sequence 45	13	0	1	0	0
Sequence 46	13	0	1	0	0
Sequence 47	13	0	1	0	0
Sequence 48	13	0	1	0	0
Sequence 49	13	0	1	0	0
Sequence 50	13	0	1	0	0
Sequence 51	13	0	1	0	0
Sequence 52	13	0	1	0	0
Sequence 53	13	0	1	0	0
Sequence 54	13	0	1	0	0
Sequence 55	13	0	1	0	0
Sequence 56	13	0	1	0	0
Sequence 57	13	0	1	0	0
Sequence 58	13	0	1	0	0
Sequence 59	13	0	1	0	0
Sequence 60	13	0	1	0	0
Sequence 61	13	0	1	0	0
Sequence 62	13	0	1	0	0
Sequence 63	13	0	1	0	0
Sequence 64	13	0	1	0	0
Sequence 65	13	0	1	0	0
Sequence 66	13	0	1	0	0
Sequence 67	13	0	1	0	0
Sequence 68	13	0	1	0	0
Sequence 69	13	0	1	0	0
Sequence 70	13	0	1	0	0
Sequence 71	13	0	1	0	0
Sequence 72	13	0	1	0	0
Sequence 73	13	0	1	0	0
Sequence 74	13	0	1	0	0
Sequence 75	13	0	1	0	0
Sequence 76	13	0	1	0	0
Sequence 77					

1233 TTAAATTTCATT 1246

14 TAAATTTTCAAT 1

SULT 837

1357217C
ABT35721 standard; DNA; 17 BP.
ABT35721;
12-JUN-2003 (first entry)
Tumour suppression related human fukutin oligo SEQ ID No 1358.
Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
antitense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
schizophrenia; protein chip; gene therapy; tumour suppression;
human fukutin; ds.

16-MAY-2001:

16-MAY-2000. 2000HS-0575031

1703/EO-SC00002; 0002-TTT-OT

(KIBO-) RIBOZIME PHARM INC.
(GLAX) GLAXO GROUP LTD

WPT. 2002-082885/12

TT/EE66700-2007;TJM

WPI; 2003-313353/30.

Disclosure: Page 191: 720pp: French.

The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (antisense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of vital diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention.

Sequence 17 BP: 10 A: 3 C: 1 G: 3 T: 0 other:

Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1146 ATTTATTATTAGAT 1159
 |||||
 DB 15 ATTTATTATTAGAT 2

RESULT 838
 ABT36211
 ID ABT36211 standard; DNA; 17 BP.
 AC ABT36211;
 XX ABT36211;
 DT 12-JUN-2003 (first entry)
 XX Tumour suppression related human fukutin oligo SEQ ID No 1848.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX Homo sapiens.
 OS
 XX WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB04208.
 XX 17-SEP-2001; 2001FR-0011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX New isolated nucleic acid, useful for treating viral diseases
 PT associated with tumors and cell degeneration, also related
 PT polypeptides, antibodies and transfected cells -
 PS Disclosure; Page 249; 720pp; French.
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 XX related human fukutin oligonucleotide of the invention.
 SQ Sequence 17 BP; 5 A; 2 C; 6 G; 4 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TCACAGTGTGTTG 966
 |||||
 DB 3 TCACAGTGTGTTAG 16

RESULT 839
 ABT36218/c
 ID ABT36218 standard; DNA; 17 BP.
 AC ABT36218;
 XX ABT36218;
 DT 12-JUN-2003 (first entry)
 XX Tumour suppression related human fukutin oligo SEQ ID No 1855.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX Homo sapiens.
 OS
 XX WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB04208.
 XX 17-SEP-2001; 2001FR-0011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX New isolated nucleic acid, useful for treating viral diseases
 PT associated with tumors and cell degeneration, also related
 PT polypeptides, antibodies and transfected cells -
 PS Disclosure; Page 249; 720pp; French.
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 XX related human fukutin oligonucleotide of the invention.
 SQ Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 413 CCAGGATCAGTGA 426
b 16 CCAGGATCAGTGA 3

RESULT 840
BT36376
D ABT36376 standard; DNA; 17 BP.

X ABT36376;
X 12-JUN-2003 (first entry)

T Tumour suppression related human fukutin oligo SEQ ID No 2013.

X Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
X antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
X schizophrenia; protein chip; gene therapy; tumour suppression;
X human fukutin; ds.

X Homo sapiens.

X WO2003025175-A2.

X 27-MAR-2003.

X 17-SEP-2002; 2002WO-IB04208.

X 17-SEP-2001; 2001FR-0011978.

X (MOLE-) MOLECULAR ENGINES LAB.

X Telerman A, Amson R, Tuijnder M;

X WPI; 2003-313353/30.

X New isolated nucleic acid, useful for treating viral diseases
X associated with tumors and cell degeneration, also related
X polypeptides, antibodies and transfected cells -

X Disclosure; Page 268; 720pp; French.

The invention relates to a novel isolated 17 mer nucleic acid sequence,
given in the specification, a sequence containing at least 15
consecutive nucleotides from the 17 mer sequence, a sequence with, after
optimal alignment, at least 80 % identity to the 17 mer sequence, a
sequence that hybridizes to them under highly stringent conditions, or
the complement of any of them, or the corresponding RNA. The novel
isolated nucleic acids of the invention are useful as probes and primers
for detecting, identifying, quantifying and/or amplifying a nucleic acid,
e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
and for production of recombinant polypeptides. Any of the nucleic acids,
polypeptides, vectors containing the nucleic acids, cells containing the
vector or antibodies directed against the polypeptides are useful for
preparation of pharmaceuticals for prevention and/or treatment of viral
diseases that are characterized by development of tumours or cell
degeneration, specifically cancer but also Alzheimer's disease and
schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
patient samples is useful for diagnosis and/or prognosis of these
diseases. The polypeptides can also be used to generate antibodies, and
both the polypeptide and antibodies are useful as components of protein
chips. The nucleic acid sequences of the invention can be used in gene
therapy. This polynucleotide sequence represents a tumour suppression
related human fukutin oligonucleotide of the invention.

Sequence 17 BP; 4 A; 1 C; 1 G; 11 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1142 ATTATTTTATTTT 1155

Db 2 ATCTATTATTTT 15

RESULT 841
ABT37154
ID ABT37154 standard; DNA; 17 BP.

XX ABT37154;

XX 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 2791.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.

XX Homo sapiens.

XX WO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB04208.

XX 17-SEP-2001; 2001FR-0011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases
XX associated with tumors and cell degeneration, also related
XX polypeptides, antibodies and transfected cells -

XX Disclosure; Page 359; 720pp; French.

The invention relates to a novel isolated 17 mer nucleic acid sequence,
given in the specification, a sequence containing at least 15
consecutive nucleotides from the 17 mer sequence, a sequence with, after
optimal alignment, at least 80 % identity to the 17 mer sequence, a
sequence that hybridizes to them under highly stringent conditions, or
the complement of any of them, or the corresponding RNA. The novel
isolated nucleic acids of the invention are useful as probes and primers
for detecting, identifying, quantifying and/or amplifying a nucleic acid,
e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
and for production of recombinant polypeptides. Any of the nucleic acids,
polypeptides, vectors containing the nucleic acids, cells containing the
vector or antibodies directed against the polypeptides are useful for
preparation of pharmaceuticals for prevention and/or treatment of viral
diseases that are characterized by development of tumours or cell
degeneration, specifically cancer but also Alzheimer's disease and
schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
patient samples is useful for diagnosis and/or prognosis of these
diseases. The polypeptides can also be used to generate antibodies, and
both the polypeptide and antibodies are useful as components of protein
chips. The nucleic acid sequences of the invention can be used in gene
therapy. This polynucleotide sequence represents a tumour suppression
related human fukutin oligonucleotide of the invention.

Sequence 17 BP; 2 A; 3 C; 1 G; 11 T; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 908 TCTCTTTTATTTCT 921

Db 3 TCTCTTTTATTTCT 16

RESULT 842
 ABT37510 standard; DNA; 17 BP.
 ID ABT37510; (first entry)
 AC ABT37510;
 XX 12-JUN-2003
 XX Tumour suppression related human fukutin oligo SEQ ID No 3147.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 XX schizophrenia; protein chip; gene therapy; tumour suppression;
 XX human fukutin; ds.
 XX Homo sapiens.
 XX WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB04208.
 XX 17-SEP-2001; 2001FR-0011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX New isolated nucleic acid, useful for treating viral diseases
 XX associated with tumors and cell degeneration, also related
 XX polypeptides, antibodies and transfected cells -
 XX Disclosure; Page 401; 720pp; French.
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 XX given in the specification, a sequence containing at least 15
 XX consecutive nucleotides from the 17 mer sequence, a sequence with, after
 XX optimal alignment, at least 80 % identity to the 17 mer sequence, a
 XX sequence that hybridizes to them under highly stringent conditions, or
 XX the complement of any of them, or the corresponding RNA. The novel
 XX isolated nucleic acids of the invention are useful as probes and primers
 XX for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 XX e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 XX and for production of recombinant polypeptides. Any of the nucleic acids,
 XX polypeptides, vectors containing the nucleic acids, cells containing the
 XX vector or antibodies directed against the polypeptides are useful for
 XX preparation of pharmaceuticals for prevention and/or treatment of viral
 XX diseases that are characterised by development of tumours or cell
 XX degeneration, specifically cancer but also Alzheimer's disease and
 XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 XX patient samples is useful for diagnosis and/or prognosis of these
 XX diseases. The polypeptides can also be used to generate antibodies, and
 XX both the polypeptide and antibodies are useful as components of protein
 XX chips. The nucleic acid sequences of the invention can be used in gene
 XX therapy. This polynucleotide sequence represents a tumour suppression
 XX related human fukutin oligonucleotide of the invention.
 XX Sequence 17 BP; 4 A; 3 C; 2 G; 8 T; 0 other;
 Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5,1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 910 TCCTTATTTCTAA 923
 DB 3 TCCTTATTTCTGA 16

RESULT 843
 ABT37886 standard; DNA; 17 BP.
 ID ABT37886;
 AC ABT37886;
 XX 12-JUN-2003 (first entry)
 XX Tumour suppression related human fukutin oligo SEQ ID No 3523.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 XX schizophrenia; protein chip; gene therapy; tumour suppression;
 XX human fukutin; ds.
 XX Homo sapiens.
 XX WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB04208.
 XX 17-SEP-2001; 2001FR-0011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX New isolated nucleic acid, useful for treating viral diseases
 XX associated with tumors and cell degeneration, also related
 XX polypeptides, antibodies and transfected cells -
 XX Disclosure; Page 445; 720pp; French.
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 XX given in the specification, a sequence containing at least 15
 XX consecutive nucleotides from the 17 mer sequence, a sequence with, after
 XX optimal alignment, at least 80 % identity to the 17 mer sequence, a
 XX sequence that hybridizes to them under highly stringent conditions, or
 XX the complement of any of them, or the corresponding RNA. The novel
 XX isolated nucleic acids of the invention are useful as probes and primers
 XX for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 XX e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 XX and for production of recombinant polypeptides. Any of the nucleic acids,
 XX polypeptides, vectors containing the nucleic acids, cells containing the
 XX vector or antibodies directed against the polypeptides are useful for
 XX preparation of pharmaceuticals for prevention and/or treatment of viral
 XX diseases that are characterised by development of tumours or cell
 XX degeneration, specifically cancer but also Alzheimer's disease and
 XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 XX patient samples is useful for diagnosis and/or prognosis of these
 XX diseases. The polypeptides can also be used to generate antibodies, and
 XX both the polypeptide and antibodies are useful as components of protein
 XX chips. The nucleic acid sequences of the invention can be used in gene
 XX therapy. This polynucleotide sequence represents a tumour suppression
 XX related human fukutin oligonucleotide of the invention.
 XX Sequence 17 BP; 6 A; 2 C; 4 G; 5 T; 0 other;
 Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5,1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 839 TCTGTTAAATCTGG 852
 DB 3 TCTGTTAAATCAGG 16

RESULT 844
 ABT38326/c

D ABT38326 standard; DNA; 17 BP.
 X C ABT38326;
 X T 12-JUN-2003 (first entry)
 X X Tumour suppression related human fukutin oligo SEQ ID No 3963.
 X C Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 X C antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 X C schizophrenia; protein chip; gene therapy; tumour suppression;
 X C human fukutin; ds.
 X C Homo sapiens.
 X C WO2003025175-A2.
 X C 27-MAR-2003.
 X C 17-SEP-2002; 2002WO-IB04208.
 X C 17-SEP-2001; 2001PR-0011978.
 X C (MOLE-) MOLECULAR ENGINES LAB.
 X C Telerman A, Amson R, Tuijnder M;
 X C WPI; 2003-313353/30.
 X C New isolated nucleic acid, useful for treating viral diseases
 X C associated with tumors and cell degeneration, also related
 X C polypeptides, antibodies and transfected cells -
 X C Disclosure; Page 497; 720pp; French.
 X C The invention relates to a novel isolated 17 mer nucleic acid sequence,
 X C given in the specification, a sequence containing at least 15
 X C consecutive nucleotides from the 17 mer sequence, a sequence with, after
 X C optimal alignment, at least 80 % identity to the 17 mer sequence, a
 X C sequence that hybridizes to them under highly stringent conditions, or
 X C the complement of any of them, or the corresponding RNA. The novel
 X C isolated nucleic acids of the invention are useful as probes and primers
 X C for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 X C e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 X C and for production of recombinant polypeptides. Any of the nucleic acids,
 X C polypeptides, vectors containing the nucleic acids, cells containing the
 X C vector or antibodies directed against the polypeptides are useful for
 X C preparation of pharmaceuticals for prevention and/or treatment of viral
 X C diseases that are characterised by development of tumours or cell
 X C degeneration, specifically cancer but also Alzheimer's disease and
 X C schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 X C patient samples is useful for diagnosis and/or prognosis of these
 X C diseases. The polypeptides can also be used to generate antibodies, and
 X C both the polypeptide and antibodies are useful as components of protein
 X C chips. The nucleic acid sequences of the invention can be used in gene
 X C therapy. This polynucleotide sequence represents a tumour suppression
 X C related human fukutin oligonucleotide of the invention.
 X C Sequence 17 BP; 8 A; 1 C; 1 G; 7 T; 0 other;
 X C Query Match 1.0%; Score 12.4; DB 1; Length 17;
 X C Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 X C Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 X C 1146 ATTTTATTATTAGAT 1159
 X C |||||
 X C 15 ATTTTATTATTAGAT 2
 X C
 X C SULT 845
 X C T39589
 X C ABT39589 standard; DNA; 17 BP.

AC ABT39589;
 XX 12-JUN-2003 (first entry)
 DT Tumour suppression related human fukutin oligo SEQ ID No 5226.
 DE Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 XX schizophrenia; protein chip; gene therapy; tumour suppression;
 XX human fukutin; ds.
 XX Homo sapiens.
 XX WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB04208.
 XX 17-SEP-2001; 2001PR-0011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 PI WPI; 2003-313353/30.
 DR New isolated nucleic acid, useful for treating viral diseases
 XX associated with tumors and cell degeneration, also related
 XX polypeptides, antibodies and transfected cells -
 XX Disclosure; Page 644; 720pp; French.
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.
 XX Sequence 17 BP; 4 A; 2 C; 4 G; 7 T; 0 other;
 SQ Query Match 1.0%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 5.1e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 809 TCAAAATTTAGCTGG 822
 |||||
 Db 3 TCAAAATTTGCTGG 16
 |||||
 RESULT 846
 ID ACA06849
 ID ACA06849 standard; RNA; 17 BP.
 XX ACA06849;
 AC ACA06849;
 XX

T 03-JUN-2003 (first entry)

X E NFKB sub-unit modulating inozyme substrate #668.
X X
X Z Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
W G-cleaver; amberzyme; cancer; REL-A activity; breast cancer;
W lung cancer; prostate cancer; colorectal cancer; brain cancer;
W oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
W lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
W chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
W cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
W gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
W rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
W gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
W transplant/graft rejection; reperfusion injury; glomerulonephritis;
W allergic airway inflammation; inflammatory bowel disease; infection;
W SS.

X S Homo sapiens.

X S US2002177568-A1.

X D 28-NOV-2002.

X F 23-MAY-2001; 2001US-0864785.

X X 15-AUG-1994; 94US-0291932.

X R 07-DEC-1992; 92US-0987132.

X R 18-MAY-1994; 94US-0245466.

X R 23-DEC-1996; 96US-0777916.

X X (STIN/) STINCHOMB D T.

X A (MCSW/) MCSWIGGEN J.

X A (DRAP/) DRAPER K G.

X I Stinchcomb DT, Mcswiggen J, Draper KG;

X X WPI; 2003-340953/32.

X X Novel enzymatic nucleic acid molecules which down regulates expression

X X of a sequence encoding a subunit of nuclear factor kappa B useful for

X X treating cancer, inflammatory disorders and autoimmune diseases -

X X Claim 3; Page 36; 72pp; English.

X X The invention describes an enzymatic nucleic acid molecule (I) which down

X X regulates expression of a sequence encoding a subunit of nuclear factor

X X kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme

X X cancer and is useful for down-regulating REL-A activity in a cell, for

X X treating a patient having a condition associated with the level of REL-A.

X X (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in

X X the presence of a divalent cation, especially Mg²⁺. The enzymatic and

X X antisense nucleic acid molecules are useful for treating breast, lung,

X X prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,

X X cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or

X X multidrug resistant cancer. The method involves use of other drug

X X therapies such as monoclonal antibodies, REL-A-specific inhibitors or

X X chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,

X X cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,

X X gemcitabine or radiation therapy. The enzymatic and antisense nucleic

X X acid molecules are also useful for treating inflammatory disease such as

X X rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,

X X rejection, autoimmune disease, lupus, multiple sclerosis, transplant/graft

Query Match 1.0%; Score 12.4; DB 1; Length 17;

Best Local Similarity 85.7%; Pred. NO. 5.1e-02;

Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 870 CCAGGATCCACAG 883

DB 1 CCAGGATCCACAG 14

RESULT 847

ACA08322

ID ACA08322 standard; DNA; 17 BP.

XX ACA08322;

DT 03-JUN-2003 (first entry)

DE Necrosis factor kappa B (NFKB) sub-unit modulating DNzyme #91.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;

XX G-cleaver; amberzyme; cancer; REL-A activity; breast cancer;

XX lung cancer; prostate cancer; colorectal cancer; brain cancer;

XX oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;

XX cervical cancer; head and neck cancer; ovarian cancer; melanoma;

XX lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;

XX chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;

XX cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;

XX gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;

XX rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;

XX gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;

XX transplant/graft rejection; reperfusion injury; glomerulonephritis;

XX allergic airway inflammation; inflammatory bowel disease; infection;

XX SS.

XX Synthetic.

OS US2002177568-A1.

PN 28-NOV-2002.

PD 23-MAY-2001; 2001US-0864785.

PF 15-AUG-1994; 94US-0291932.

PR 07-DEC-1992; 92US-0987132.

PR 18-MAY-1994; 94US-0245466.

PR 23-DEC-1996; 96US-0777916.

XX (STIN/) STINCHOMB D T.

XX (MCSW/) MCSWIGGEN J.

XX (DRAP/) DRAPER K G.

PI Stinchcomb DT, Mcswiggen J, Draper KG;

XX WPI; 2003-340953/32.

XX Novel enzymatic nucleic acid molecules which down regulates expression

XX of a sequence encoding a subunit of nuclear factor kappa B useful for

XX treating cancer, inflammatory disorders and autoimmune diseases -

XX Claim 3; Page 48; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down

XX regulates expression of a sequence encoding a subunit of nuclear factor

XX kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme

XX cancer and is useful for down-regulating REL-A activity in a cell, for

C therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents an enzymatic nucleic acid used to modulate the function of a necrosis factor kappa B sub-unit.

Sequence 17 BP; 5 A; 5 C; 4 G; 3 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 5.1e+02;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

870 CCAGGATCCACAAG 883
4 CCAGGATCCACAAG 17

SUIT 848

ABZ60207
ABZ60207 standard; RNA; 17 BP.

ABZ60207;

21-MAR-2003 (first entry)

Human K-Ras DNAzyme substrate #319.

Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras; enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV; anti-rheumatic; cancer; AIDS; ss.

Homo sapiens.

WO200297114-A2.

05-DEC-2002.

29-MAY-2002; 2002WO-US16840.

29-MAY-2001; 2001US-294140P.

06-JUN-2001; 2001US-296249P.

10-SEP-2001; 2001US-318471P.

(RIBO-) RIBOZYME PHARM INC.

McSwiggen J;

WPI; 2003-140484/13.

Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

Claim 58; Page 91; 185pp; English.

The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target

CC sequences for the human ribozymes of the invention.

XX Sequence 17 BP; 8 A; 3 C; 1 G; 5 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 5.1e+02;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1175 ATTAGTAAATTC 1188

DB 4 AUAAGUAAAUUAC 17

RESULT 349

ABZ61180

ID ABZ61180 standard; RNA; 17 BP.

XX AC ABZ61180;

DT 21-MAR-2003 (first entry)

Human K-Ras DNAzyme substrate #1292.

Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras; enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV; anti-rheumatic; cancer; AIDS; ss.

Homo sapiens.

WO200297114-A2.

05-DEC-2002.

29-MAY-2002; 2002WO-US16840.

29-MAY-2001; 2001US-294140P.

06-JUN-2001; 2001US-296249P.

10-SEP-2001; 2001US-318471P.

(RIBO-) RIBOZYME PHARM INC.

McSwiggen J;

WPI; 2003-140484/13.

Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

Claim 58; Page 109; 185pp; English.

The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target sequences for the human ribozymes of the invention.

Sequence 17 BP; 7 A; 0 C; 3 G; 7 U; 0 other;

Query Match 1.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 5.1e+02;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1111 TCATTCATAGTTA 1124

DB 2 UAAUUGAUAUUA 15

RESULT 850
AA66457/C
D AAA66457 standard; DNA; 25 BP.
X
X AAA66457;
X
X 09-OCT-2000 (first entry)
X
E Dog genomic marker oligonucleotide sequence SEQ ID NO:319.
X
X Dog; genome; genomic marker; radiation hybrid map; identification;
W chromosome location; gene marker; polymorphic microsatellite marker;
W phenotype; behaviour; pedigree; ss.
X
X Canis familiaris.
X
X WO200029615-A2.
X
X 25-MAY-2000.
D
D 15-NOV-1999; 99WO-IB01907.
F
X 13-NOV-1998; 98US-0108193.
R
X (CNRS) CNRS CENT NAT RECH SCI.
A Galibert P, Andre C;
H WPI; 2000-387821/33.
R
X New radiation hybrid map of the dog, Canine familiaris, genome, useful
T for e.g. identifying genes implicated in phenotypic and behavioral
T traits or in genetic diseases and for studying dog pedigrees -
X
X Claim 1; Page 66; 87pp; English.
X
X The present invention describes a radiation hybrid map of the dog
X (Canine familiaris) genome comprising the genome location of a marker
X selected from AAA66139 to AAA66942. The radiation hybrid map is useful
X for identifying and localising dog genes, since it covers approximately
X 80 % of the dog genome and provides a dense map integrating different
X types (i.e. Type I and Type II) of markers. The map and the dog genome
X markers (or complementary sequences) are especially useful to identify
X genes responsible for phenotypic and behavioural traits in dogs, to
X identify morbid genes, to analyse diseases and identify implicated genes
X in such diseases and their alleles, and to study dog pedigrees. They
X may also be useful for isolating corresponding human gene sequences
X e.g. genes involved in genetic diseases.
X
X Sequence 25 BP; 12 A; 5 C; 3 G; 5 T; 0 other;
X
Query Match 1.0%; Score 12.4; DB 1; Length 25;
Best Local Similarity 72.7%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
X
QY 1008 TAAATTTTTCAGCTGTAACCT 1029
DB 25 TAGATTTTTCAGCTCTCATT 4
X
RESULT 851
AAL55125/C
ID AAL55125 standard; DNA; 30 BP.
X
X AAL55125;
AC AAL55125;
X
X 16-APR-2003 (first entry)
DF
DE Nucleic acid synthesising method related PCR primer, SEQ ID NO 6.
X
X Synthesising; target base sequence; annealing; genetic disease; SNP;
KW

KW single nucleotide polymorphism; cancer; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200290538-A1.
XX
PD 14-NOV-2002.
XX
XX 08-MAY-2002; 2002WO-JP04479.
XX
XX 08-MAY-2001; 2001JP-0137060.
PR 18-JUN-2001; 2001JP-0184131.
PR
XX (BIKE) EIKEN KAGAKU KK.
PA
XX Nagamine K;
XX PI
XX DR
XX WPI; 2003-120547/11.
XX
XX Synthesizing target base sequence-containing nucleic acids constituting
PT complementary base sequences against template by the LAMP method,
PT applicable in identifying genetic diseases, cancerization and
PT microorganisms -
XX
PS Example 1; Page 62; 107pp; Japanese.
XX
XX The invention relates to a novel method for synthesising a target base
CC sequence-containing nucleic acids. The method comprises the formation of
CC single-stranded nucleic acids; synthesis of complementary strand by
CC annealing; and producing single-stranded nucleic acid from a target base
CC sequence by the synthesis of a complementary strand by annealing of a
CC complementary base sequence. The method is useful for synthesising a
CC target base sequence-containing nucleic acids, which is applicable in
CC detecting SNP (single nucleotide polymorphism) in genes, identifying
CC genetic diseases, cancer and microorganisms. Such a method can be
CC easily, rapidly and freely carried out without being influenced by
CC contamination or complicated temperature control, but with improved
CC reaction specificity, high accuracy and efficiency, operable at low cost.
CC This polynucleotide sequence represents a PCR primer used in the
CC synthesising method of the invention.
XX
SQ Sequence 30 BP; 13 A; 3 C; 5 G; 9 T; 0 other;
X
Query Match 1.0%; Score 12.4; DB 1; Length 30;
Best Local Similarity 72.7%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
X
QY 1068 CAAATATTTTGTGCAAGATTTG 1089
DB 25 CAAATCTTGTGCAAGATTTG 4
X
RESULT 852
AAA22700/C
ID AAA22700 standard; RNA; 17 BP.
XX
XX AAA22700;
AC
XX
XX 19-JUN-2000 (first entry)
XX
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:5926.
X
X Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cycostatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus sclerosis; pot-wire stain; Sturge Weber syndrome;
KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
OS

KW WO9950403-A2.
 XX 07-OCT-1999.
 XX 24-MAR-1999; 99WO-US06507.
 XX 27-MAR-1998; 98US-0079678.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 XX Novel ribozymes for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding an angiogenic factors -
 XX Claim 54; Page 237; 305pp; English.
 XX The present invention describes enzymatic cleavage of nucleic acid molecules with
 XX RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 XX gene, an integrin alpha 5 subunit gene, or a Tie-2 gene. AAL16775 to
 XX AAL17167 and AAL17561 to AAL17622 represent ribozyme sequences for ARNT,
 XX and AAL17168 to AAL17560 and AAL17623 to AAL17684 represent their
 XX corresponding target sequences; AAL17685 to AAL18385 and AAL19087 to
 XX AAL19154 represent ribozyme sequences for Tie-2, and AAL18386 to AAL19086
 XX and AAL19155 to AAL19222 represent their corresponding target sequences;
 XX AAL19223 to AAL20361 and AAL21501 to AAL21595 represent ribozyme
 XX sequences for integrin alpha 6 subunit, and AAL20362 to AAL21500 and
 XX AAL21596 to AAL21688 represent their corresponding target sequences;
 XX AAL21689 to AAL22475 and AAL23263 to AAL23342 represent ribozyme sequences
 XX for integrin subunit beta 3, and AAL22476 to AAL23262, AAL23343 to
 XX AAL23422 represent their corresponding target sequences. The ribozymes of
 XX the invention are used for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding angiogenic factor, especially ARNT,
 XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 XX especially used to treat cancer, diabetic retinopathy, age related
 XX macular degeneration (ARMD), inflammation, and arthritis, as well as
 XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 XX angiobroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
 XX integrin subunit alpha-6, or integrin subunit beta-3.
 XX Sequence 17 BP; 4 A; 0 C; 0 G; 13 U; 0 other;
 XX
 XX Query Match 1.0%; Score 12.2; DB 1; Length 17;
 XX Best Local Similarity 82.4%; Pred. No. 5.5e+02;
 XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX 1590 AAATATAAAGTAATA 1606
 XX 17 AAATAATAATAATA 1
 XX
 XX LT 853
 XX 2703/c
 XX AAA22703 standard; RNA; 17 BP.
 XX AAA22703;
 XX
 XX 19-JUN-2000 (first entry)
 XX Integrin subunit beta 3 substrate sequence SEQ ID NO:5929.
 XX
 XX Human; aryl hydrocarbon nuclear transporter; ARNT; TIE-2; angiogenesis;
 XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 XX ophthalmologic; antiinflammatory; antiarthritis; antipsoriatic; ARMD;
 XX dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 XX age related macular degeneration; inflammation; neovascular glaucoma;
 XX
 XX RESULT 854
 XX AAA22706/c
 XX ID AAA22706 standard; RNA; 17 BP.
 XX XX AAA22706;
 XX AC AAA22706;
 XX XX
 XX DT 19-JUN-2000 (first entry)
 XX XX Integrin subunit beta 3 substrate sequence SEQ ID NO:5932.
 XX DB
 XX XX Human; aryl hydrocarbon nuclear transporter; ARNT; TIE-2; angiogenesis;
 XX KW

KW WO9950403-A2.
 XX 07-OCT-1999.
 XX 24-MAR-1999; 99WO-US06507.
 XX 27-MAR-1998; 98US-0079678.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 XX Novel ribozymes for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding an angiogenic factors -
 XX Claim 54; Page 237; 305pp; English.
 XX The present invention describes enzymatic cleavage of nucleic acid molecules with
 XX RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 XX gene, an integrin alpha 5 subunit gene, or a Tie-2 gene. AAL16775 to
 XX AAL17167 and AAL17561 to AAL17622 represent ribozyme sequences for ARNT,
 XX and AAL17168 to AAL17560 and AAL17623 to AAL17684 represent their
 XX corresponding target sequences; AAL17685 to AAL18385 and AAL19087 to
 XX AAL19154 represent ribozyme sequences for Tie-2, and AAL18386 to AAL19086
 XX and AAL19155 to AAL19222 represent their corresponding target sequences;
 XX AAL19223 to AAL20361 and AAL21501 to AAL21595 represent ribozyme
 XX sequences for integrin alpha 6 subunit, and AAL20362 to AAL21500 and
 XX AAL21596 to AAL21688 represent their corresponding target sequences;
 XX AAL21689 to AAL22475 and AAL23263 to AAL23342 represent ribozyme sequences
 XX for integrin subunit beta 3, and AAL22476 to AAL23262, AAL23343 to
 XX AAL23422 represent their corresponding target sequences. The ribozymes of
 XX the invention are used for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding angiogenic factor, especially ARNT,
 XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 XX especially used to treat cancer, diabetic retinopathy, age related
 XX macular degeneration (ARMD), inflammation, and arthritis, as well as
 XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 XX angiobroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
 XX integrin subunit alpha-6, or integrin subunit beta-3.
 XX Sequence 17 BP; 4 A; 0 C; 0 G; 13 U; 0 other;
 XX
 XX Query Match 1.0%; Score 12.2; DB 1; Length 17;
 XX Best Local Similarity 82.4%; Pred. No. 5.5e+02;
 XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX 1590 AAATATAAAGTAATA 1606
 XX 17 AAATAATAATAATA 1
 XX
 XX LT 853
 XX 2703/c
 XX AAA22703 standard; RNA; 17 BP.
 XX AAA22703;
 XX
 XX 19-JUN-2000 (first entry)
 XX Integrin subunit beta 3 substrate sequence SEQ ID NO:5929.
 XX
 XX Human; aryl hydrocarbon nuclear transporter; ARNT; TIE-2; angiogenesis;
 XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 XX ophthalmologic; antiinflammatory; antiarthritis; antipsoriatic; ARMD;
 XX dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 XX age related macular degeneration; inflammation; neovascular glaucoma;
 XX

1 integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 2 hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
 3 ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 4 dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 5 age related macular degeneration; inflammation; verruca vulgaris; glaucoma;
 6 myopic degeneration; psoriasis; verruca vulgaris; angioblastoma;
 7 tuberculous scleriosis; pot-wine stain; Sturge Weber syndrome;
 8 Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 9 Homo sapiens.
 10 WO9950403-A2.
 11 07-OCT-1999.
 12 24-MAR-1999; 99WO-US06507.
 13 27-MAR-1998; 98US-0079678.
 14 (RIBO-) RIBOZYME PHARM INC.
 15 Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 16 WPI; 1999-591315/50.
 17 Novel ribozymes for modulating the synthesis, expression and/or
 18 stability of an mRNA encoding an angiogenic factors -
 19 Claim 54; Page 237; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with
 RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 and AAA19155 to AAA19222 represent their corresponding target sequences;
 AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 AAA21596 to AAA21688 represent their corresponding target sequences;
 AAA21689 to AAA22475 and AAA22476 to AAA23262, AAA23343 to
 AAA23422 represent their corresponding target sequences. The ribozymes of
 the invention are used for modulating the synthesis, expression and/or
 stability of an mRNA encoding angiogenic factor, especially ARNT,
 integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 especially used to treat cancer, diabetic retinopathy, age related
 macular degeneration (ARMD), inflammation, and arthritis, as well as
 neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 angioblastoma of tuberculous scleriosis, pot-wine stains, Sturge Weber
 syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 and other syndromes and diseases related to the levels of ARNT, Tie-2,
 integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 4 A; 0 C; 0 G; 13 U; 0 other;
 Query Match 1.0%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 5.5e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1590 AAATATAAAGTAATA 1606
 17 AAATATAAAGTAATA 1

ULT 855
 22899
 AAA22899 standard; RNA; 17 BP.
 AAA22899;

DT 19-JUN-2000 (first entry)
 XX Integrin subunit beta 3 substrate sequence SEQ ID NO:6125.
 DE Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
 XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; verruca vulgaris; glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angioblastoma;
 KW tuberculous scleriosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 OS WO9950403-A2.
 XX 07-OCT-1999.
 XX 24-MAR-1999; 99WO-US06507.
 XX 27-MAR-1998; 98US-0079678.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or
 stability of an mRNA encoding an angiogenic factors -
 Claim 54; Page 249; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with
 RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 and AAA19155 to AAA19222 represent their corresponding target sequences;
 AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 AAA21596 to AAA21688 represent their corresponding target sequences;
 AAA21689 to AAA22475 and AAA22476 to AAA23262, AAA23343 to
 AAA23422 represent their corresponding target sequences. The ribozymes of
 the invention are used for modulating the synthesis, expression and/or
 stability of an mRNA encoding angiogenic factor, especially ARNT,
 integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 especially used to treat cancer, diabetic retinopathy, age related
 macular degeneration (ARMD), inflammation, and arthritis, as well as
 neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 angioblastoma of tuberculous scleriosis, pot-wine stains, Sturge Weber
 syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 and other syndromes and diseases related to the levels of ARNT, Tie-2,
 integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 13 A; 0 C; 0 G; 4 U; 0 other;

Query Match 1.0%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 5.5e+02;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1590 AAATATAAAGTAATA 1606
 DB 1 AAATATAAAGTAATA 17

RESULT 856

AA22900
 D AAA22900 standard; RNA; 17 BP.
 C
 K AAA22900;
 K
 K 19-JUN-2000 (first entry)
 C
 C Integrin subunit beta 3 substrate sequence SEQ ID NO:6126.
 C
 C Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 C integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 C hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
 C ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 C dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 C age related macular degeneration; inflammation; neovascular glaucoma;
 C myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 C tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 C Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 C Homo sapiens.
 C WO9950403-A2.
 C 07-OCT-1999.
 C 24-MAR-1999; 99WO-US06507.
 C 27-MAR-1998; 98US-0079678.
 C (RIBO-) RIBOZYME PHARM INC.
 C Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 C WPI; 1999-591315/50.
 C Novel ribozymes for modulating the synthesis, expression and/or
 C stability of an mRNA encoding an angiogenic factors -
 C Claim 54; Page 249; 305pp; English.
 C The present invention describes enzymatic cleave RNA molecules with
 C RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 C hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 C gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 C AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 C and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 C corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 C AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 C and AAA19155 to AAA19222 represent their corresponding target sequences;
 C AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 C sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 C AAA21596 to AAA21688 represent their corresponding target sequences;
 C AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 C for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 C AAA23422 represent their corresponding target sequences. The ribozymes of
 C the invention are used for modulating the synthesis, expression and/or
 C stability of an mRNA encoding angiogenic factor, especially ARNT,
 C integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 C especially used to treat cancer, diabetic retinopathy, age related
 C macular degeneration (ARMD), inflammation, and arthritis, as well as
 C neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 C angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 C syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 C and other syndromes and diseases related to the levels of ARNT, Tie-2,
 C integrin subunit alpha-6, or integrin subunit beta-3.
 C Sequence 17 BP; 13 A; 0 C; 0 G; 4 U; 0 other;
 C
 C Query Match 1.0%; Score 12.2; DB 1; Length 17;
 C Best Local Similarity 64.7%; Pred. No. 5.5e+02;
 C Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 C 1590 AAATATAAAAGTAAATA 1606

Db RESULT 857
 ID AAA22901
 XX AAA22901 standard; RNA; 17 BP.
 AC AAA22901;
 XX 19-JUN-2000 (first entry)
 DT Integrin subunit beta 3 substrate sequence SEQ ID NO:6127.
 XX
 DE Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 OS WO9950403-A2.
 XX 07-OCT-1999.
 PD 24-MAR-1999; 99WO-US06507.
 PF 27-MAR-1998; 98US-0079678.
 PR (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 PI WPI; 1999-591315/50.
 DR Novel ribozymes for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding an angiogenic factors -
 XX Claim 54; Page 249; 305pp; English.
 CC The present invention describes enzymatic cleave RNA molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 CC Sequence 17 BP; 13 A; 0 C; 0 G; 4 U; 0 other;
 XX

Query Match 1.0%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 5.5e+02;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Y 1590 AAATATAAAAGTAAATA 1606
 |||:|:|:|:|:|:|:|:|:
 b 1 AAATATAAAAGTAAATA 17

RESULT 858
 D AA22902
 C AAA22902;
 X 19-JUN-2000 (first entry)
 T Integrin subunit beta 3 substrate sequence SEQ ID NO:6128.
 E Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 X integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 W hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 W ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 W dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 W age related macular degeneration; inflammation; neovascular glaucoma;
 W myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 W tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 W Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 X Homo sapiens.
 S WO9950403-A2.
 X WO9950403-A2.
 X 07-OCT-1999.

24-MAR-1999; 99WO-US06507.
 27-MAR-1998; 98US-0079678.
 (RIBO-) RIBOZYME PHARM INC.
 Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 WPI; 1999-591315/50.
 Novel ribozymes for modulating the synthesis, expression and/or
 stability of an mRNA encoding an angiogenic factors -
 Claim 54; Page 249; 305pp; English.

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 RNA cleaving activity, which specifically cleave RNA encoded by an aryl
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 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 represent their corresponding target sequences. The ribozymes of
 AAA19155 to AAA19222 represent their corresponding target sequences;
 AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 AAA21596 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequences
 for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 AAA23422 represent their corresponding target sequences. The ribozymes of
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 stability of an mRNA encoding angiogenic factor, especially ARNT.
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 especially used to treat cancer, diabetic retinopathy, age related
 macular degeneration (ARMD), inflammation, and arthritis, as well as
 neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,

CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX Sequence 17 BP; 13 A; 0 C; 0 G; 4 U; 0 other;
 SQ

Query Match 1.0%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 5.5e+02;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1590 AAATATAAAAGTAAATA 1606
 |||:|:|:|:|:|:|:|:|:
 Db 1 AAATATAAAAGTAAATA 17

RESULT 859
 AAA22903
 ID AAA22903 standard; RNA; 17 BP.

XX AAA22903;
 AC AAA22903;

XX 19-JUN-2000 (first entry)
 DT Integrin subunit beta 3 substrate sequence SEQ ID NO:6129.

XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 OS WO9950403-A2.
 XX WO9950403-A2.
 XX 07-OCT-1999.
 XX 24-MAR-1999; 99WO-US06507.
 XX 27-MAR-1998; 98US-0079678.
 FR (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 PI WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or
 stability of an mRNA encoding an angiogenic factors -
 Claim 54; Page 249; 305pp; English.
 The present invention describes enzymatic cleavage of nucleic acid molecules with
 RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 represent their corresponding target sequences. The ribozymes of
 AAA19155 to AAA19222 represent their corresponding target sequences;
 AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 AAA21596 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequences
 for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 AAA23422 represent their corresponding target sequences. The ribozymes of
 the invention are used for modulating the synthesis, expression and/or
 stability of an mRNA encoding angiogenic factor, especially ARNT,
 integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are

The method is also used to show the progression of diabetes mellitus in a patient suffering from the disease. This sequence represents a *Saccharomyces cerevisiae* PAF-AH DNA related oligonucleotide.

Sequence 18 BP; 4 A; 1 C; 4 G; 9 T; 0 other;

Query Match 1.0%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 5.8e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1247 CAGATAAACACAAATA 1263

```

Db      ||||| ||||| ||||| |||||
        17 CAGATACCAATAATTA 1

RESULT 862
ID      AAQ20160 standard; DNA; 18 BP.
XX
XX
XX      AAQ20160;
XX
XX      01-APR-1992 (first entry)
XX
XX      Cross-linking oligomer 723 to target Herpes Simplex Virus 1.
XX
XX      deoxyribonucleic acid; major groove; HSV;
XX      inverted polarity region; covalent cross-linking group; ss.
XX
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      modified_base 1
XX      /tag= a
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 2
XX      /tag= b
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 3
XX      /tag= c
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 4
XX      /tag= d
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 5
XX      /tag= e
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 6
XX      /tag= f
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 7
XX      /tag= g
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 8
XX      /tag= h
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 9
XX      /tag= i
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 10
XX      /tag= j
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 11
XX      /tag= k
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 12
XX      /tag= l
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 13
XX      /tag= m
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 14
XX      /tag= n
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 15
XX      /tag= o
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 16
XX      /tag= p
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX      modified_base 17
XX      /tag= q
XX      /mod_base= OTHER
XX      /note= "N-methyl-8-oxo-2'-deoxyadenine"

New sequence-specific non-photo-activated crosslinking agents -
bind to the major groove of duplex DNA and are esp. useful for
treating latent infections e.g. HIV

Example 4; Page 29; 42pp; English.

This oligomer contains an inverted polarity region formed from an
o-xyloso dimer synthon. Residues 11 and 12 are linked via an
o-xyloso group (i.e. nucleotides that have xylose sugar linked via
the o-xyloso ring). The sequence is designed to target the Herpes
Simplex virus 1 beginning at nucleotide 10996 and to covalently
cross-link to it. See also AAQ20151-Q20161.

Sequence 18 BP; 13 A; 0 C; 0 G; 5 T; 0 other;
Query Match      1.0%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1045 TATTATGCTATTTATTT 1061
Db      17 TATTATTTATTTATTT 1

RESULT 863
ID      AAQ30310 standard; DNA; 18 BP.
XX
XX      AAQ30310;
XX
XX      25-MAR-2003 (updated)
XX      07-DEC-1992 (first entry)
XX
XX      Oligomer HSV723 for forming triplex with HSV target duplex.
XX
XX      Herpes simplex virus 1; AIDS; modified; HIV; RSV; HPV; malignancy;
XX      hepatitis; inflammation; ss.
XX
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      modified_base 1
XX      /tag= a
XX      /mod_base= OTHER
XX      /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX      modified_base 2
XX      /tag= b
XX      /mod_base= OTHER
XX      /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX      modified_base 3
XX      /tag= c
XX      /mod_base= OTHER
XX      /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX      modified_base 4
XX      /tag= d
XX      /mod_base= OTHER
XX      /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

```


PT misc_feature 12..13
 PT /*tag= g
 PT /note= "O-xylosa dimer synthon linkage"
 XX
 XX WO209705-A1.
 XX
 XX 11-JUN-1992.
 XX
 XX 25-NOV-1991; 91WO-US08811.
 XX
 XX 23-NOV-1990; 90US-0617907.
 XX
 XX 18-JAN-1991; 91US-0643382.
 XX
 XX 08-APR-1991; 91US-0683420.
 XX
 XX 17-APR-1991; 91US-0686544.
 XX
 XX 17-APR-1991; 91US-0686546.
 XX
 XX 17-APR-1991; 91US-0686547.
 XX
 XX 27-SEP-1991; 91US-0766733.
 XX
 XX (GILB-) GILEAD SCI INC.
 XX
 XX Froehner B, Krawczyk S, Matteucci MD, Milligan J;
 XX WPI; 1992-217083/26.
 XX
 XX New oligomers contg. modified bases - which form a triplex with
 XX G-C doublet in a DNA duplex, for treating and diagnosing HIV,
 XX hepatitis, herpes, malignancy and inflammation
 XX
 XX Claim 12; Page 69; 77pp; English.
 XX
 XX The synthetic oligomer is capable of forming a triplex at
 XX physiological pH with a purine rich target sequence by coupling
 XX into the major groove of the duplex. The specific target sequence
 XX of this oligomer is the human interleukin-1 beta gene beginning at
 XX nucleotide 6379 contg. a purine rich sequence concd. on one strand
 XX of the duplex. The oligomer, and others like it are useful in
 XX diagnosis and therapy of diseases characterised by specific DNA
 XX duplex targets, e.g. HIV, hepatitis B, herpes, malignant
 XX tumours and inflammation. The triple helices form under mild conditions
 XX thus assays may be carried out without subjecting the test specimen to
 XX harsh conditions. The oligomer contains an inverted polarity region
 XX formed from an o-xylosa dimer synthon. The linking gp. is o-xylosa
 XX (nucleotides have the 3' positions of xylose sugars linked via the
 XX o-xylosa ring). Two nucleotides are coupled through a xylose residue
 XX to form the dimer synthon. This additional modification may render
 XX the oligomer stable to nuclease activity. The oligomer is able to
 XX inhibit gene expression, as verified by in vitro systems.
 XX See also AAQ25452-25501 and AAQ30225-448.
 XX (Updated on 25-MAR-2003 to correct FN field.)
 XX
 XX Sequence 18 BP; 5 A; 0 C; 0 G; 13 T; 0 other;
 XX
 XX Query Match 1.0%; Score 12.2; DB 1; Length 18;
 XX Best Local Similarity 82.4%; Pred. No. 5.8e+02;
 XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX 1590 AATATATAAAGTAAATA 1606
 XX 17 AATATATAAATAAATA 1
 XX
 XX RESULT 865
 XX ABZ10596
 XX ID ABZ10596 standard; DNA; 18 BP.
 XX AC ABZ10596;
 XX
 XX 16-JAN-2003 (first entry)
 XX
 XX Haematopoietic cell proliferation disorder related oligonucleotide #736.
 XX
 XX Human; haematopoietic cell proliferation disorder; cytostatic;
 XX gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KW

KW cytosine methylation state; probe; primer; ss.
 XX
 XX Homo sapiens.
 XX Synthetic.
 XX
 XX WO200277272-A2.
 XX
 XX 03-OCT-2002.
 XX
 XX 26-MAR-2002; 2002WO-EP03401.
 XX
 XX 26-MAR-2001; 2001US-278333P.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 XX Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu B;
 XX Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T;
 XX Pellet C, Schwöbe I, Ziebarth H;
 XX WPI; 2003-018942/01.
 XX
 XX Detecting and differentiating between haematopoietic cell proliferative
 XX disorders, comprises contacting a target nucleic acid with a reagent
 XX that distinguishes between methylated and non-methylated CpG
 XX dinucleotides -
 XX
 XX Claim 15; Page 52; 117pp; English.
 XX
 XX The present invention describes a method for detecting and
 XX differentiating between haematopoietic cell proliferative disorders
 XX associated with at least 1 gene and/or their regulatory regions in a
 XX subject. The method comprises contacting a target nucleic acid in a
 XX biological sample obtained from the subject with at least 1 reagent,
 XX which distinguishes between methylated and non-methylated CpG
 XX dinucleotides within the target nucleic acid. AB209861 to AB211118
 XX represent specifically claimed nucleotide sequences from the present
 XX invention. Oligonucleotides from the present invention can be used: for
 XX differentiating between healthy haematopoietic cells and proliferative
 XX disorder haematopoietic cells; for differentiating between acute
 XX lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 XX determining the cytosine methylation state and/or single nucleotide
 XX polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 XX related sequences and their complements; and as primers for the
 XX amplification of haematopoietic cell proliferation disorder related
 XX DNA sequences. The nucleotide sequences from the present invention can
 XX also be used for detecting a predisposition to, differentiation between
 XX subclasses, diagnosis, prognosis, treatment and/or monitoring of
 XX haematopoietic cell proliferative disorders. The present method enables
 XX a highly specific classification of haematopoietic cell proliferative
 XX disorders allowing for improved and informed treatment of patients.
 XX
 XX Sequence 18 BP; 3 A; 0 C; 4 G; 11 T; 0 other;
 XX
 XX Query Match 1.0%; Score 12.2; DB 1; Length 18;
 XX Best Local Similarity 82.4%; Pred. No. 5.8e+02;
 XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX 1286 TGTGTTATCTGCAATTT 1302
 XX 1 TGTGTTTTCGAAATTT 17
 XX
 XX RESULT 866
 XX ABL46342/c
 XX ID ABL46342 standard; DNA; 20 BP.
 XX AC ABL46342;
 XX
 XX 26-APR-2002 (first entry)
 XX
 XX Human interleukin-1 beta oligonucleotide SEQ ID NO:309.
 XX

Nucleic acid accessible hybridisation site; detection; hybridisation;
characterisation; identification; nucleic acid structure; diagnosis;
PCR primer; probe; ss.

Homo sapiens.
Synthetic.

WO200198537-A2.

27-DEC-2001.

15-JUN-2001; 2001WO-US19401.

17-JUN-2000; 2000US-212308P.

15-JUN-2001; 2001US-0212308.

(THIR-) THIRD WAVE TECHNOLOGIES INC.

Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;

WPI; 2002-049698/06.

Identifying oligonucleotides hybridizing to nucleic acids containing
secondary structure, useful in clinical diagnosis, comprises
identifying primers that interact with the target to form an extension
product under amplification conditions -

Claim 48; Fig 81A; 409pp; English.

The present invention describes a method for identifying oligonucleotides
with desired hybridisation properties to nucleic acid targets containing
secondary structure. The method comprises amplifying a target nucleic
acid having at least one accessible and one inaccessible site. Primers
that form an extension product are identified as the oligonucleotides
which can interact with the folded target nucleic acid. Oligonucleotides
from the present invention can be used in novel detection methods for
clinical diagnostic purposes, including the detection and identification
of pathogenic organisms (e.g. HIV). The method allows the ability to
rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
sequences used in the exemplification of the present invention.

Sequence 20 BP; 7 A; 5 C; 2 G; 6 T; 0 other;

Query Match 1.0%; Score 12.2; DB 1; Length 20;

Best Local Similarity 82.4%; Pred. No. 6.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

552 TTTTTCATGTGACCATG 568

|||||
17 TATTTTCATGGTACCATG 1

SULT 867

Z37709

AAZ37709 standard; DNA; 20 BP.

AAZ37709;

07-JAN-2000 (first entry)

Human mdm2 phosphorothioate oligodeoxynucleotide #239.

Human mdm2 gene; proliferation; tumour; phosphorothioate; p53;
cancer; antisense; modulation; oligonucleotide; expression;
inhibition; hyperproliferation; blood cancer; brain cancer;
breast cancer; lung cancer; soft tissue cancer; psoriasis; fibrosis;
atherosclerosis; restenosis; ss.

Synthetic.

Homo sapiens.

WO9949065-A1.

30-SEP-1999.

XX 26-MAR-1999; 99WO-US06702.

XX 26-MAR-1998; 98US-0048810.

XX (ISIS-) ISIS PHARM INC.

XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseert LM;

XX WPI; 1999-610754/52.

XX New antisense compounds used to treat eg. hyperproliferative conditions

PT -

XX Example 9; Page 54; 157pp; English.

XX AAZ37473-237738 represent human mdm2 phosphorothioate oligonucleotides.
CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
CC exemplification of the present invention. The present invention
CC describes novel nucleotide antisense compounds, targeted to the 5'
CC untranslated, translation termination codon, or 3' untranslated region
CC of a nucleic acid encoding human mdm2, that modulates expression of
CC human mdm2. The oligonucleotides mediate their effect by antisense
CC inhibition of hyperproliferative gene expression. The antisense compound
CC is used to treat an animal having a disease or condition associated
CC with mdm2, particularly a hyperproliferative condition, more
CC particularly cancer, especially of the blood, brain, breast, lung or soft
CC tissue, or psoriasis, fibrosis, atherosclerosis or restenosis.

XX Sequence 20 BP; 9 A; 1 C; 2 G; 8 T; 0 other;

Query Match 1.0%; Score 12.2; DB 1; Length 20;

Best Local Similarity 82.4%; Pred. No. 6.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1603 AATATGGAACATTTAAA 1619

|||||
2 AATAAGTTACATTTAAA 18

RESULT 868

AAZ29478

ID AAZ29478 standard; DNA; 20 BP.

XX AAZ29478;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31618.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
XX atherosclerosis; tumour; cytostatic; anti psoriatic;
XX anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= All phosphorothioate linkages,
FT additionally bases 1-6 and bases 15-20 are
FT 2'-O-methoxyethyl bases, and bases 7-14 are
FT deoxynucleotides"

PN US2001016575-A1.

XX 23-AUG-2001.

XX 02-JAN-2001; 2001US-0752983.

XX 26-MAR-1999; 99US-0280805.

R 26-MAR-1998; 98US-0048810.
 X (MIRA/) MIRAGLIA L J.
 A (NERO/) NERO P.
 T (GRAH/) GRAHAM M J.
 A (MONI/) MONIA B P.
 A (COWS/) COWSERT L M.
 X I Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
 X R WPI; 2001-535565/59.
 X An antisense compound, useful for treating e.g. cancer, comprises
 T nucleobases targeted a region (e.g. translation termination codon
 T region) of a nucleic acid encoding human mdm2 -
 S Example 9; Page 18; 81pp; English.
 X The present invention relates to antisense compounds, 8-30 nucleobases
 C in length targeted to the 5' untranslated region, translation
 C termination codon region, 3' untranslated region, coding region or
 C translation start site of a nucleic acid encoding human mdm2, where
 C the antisense compound modulates the expression of human mdm2. The
 C antisense oligonucleotides of the invention are useful for encoding
 C human mdm2 and for inhibiting the expression of human mdm2. They may be
 C used for treating an animal having a disease or condition associated
 C with amplification of mdm2 gene or overexpression of mdm2 e.g. a
 C hyperproliferative disorder such as cancer (blood, brain, breast, lung,
 C or a soft tissue cancer) and psoriasis, fibrosis, atherosclerosis or
 C restenosis, tumours, colorectal carcinoma and chronic myelogenous
 C leukemia. The antisense compound may be administered with a
 C chemotherapeutic agent to overcome drug resistance. The antisense
 C compound reduces hyperproliferation of human cells. The method, which
 C involves the use of the antisense compound, is also useful for detecting
 C the role of mdm2 expression in various cell functions and physiological
 C processes and useful in both clinical research and diagnostic tools.
 C AAS29242-AAS29507 represent the human mdm2 antisense oligonucleotides
 C of the present invention.
 X
 Q Sequence 20 BP; 9 A; 1 C; 2 G; 8 T; 0 other;
 Query Match 1.0%; Score 12.2; DB 1; Length 20;
 Best Local Similarity 82.4%; Pred. No. 5.2e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Y 1603 AATATGAACATTAA 1619
 b |||||
 2 AATAAGTTACATTAA 18
 RESULT 869
 AF80863
 D AAF80863 standard; DNA; 20 BP.
 X AAF80863;
 X 02-MAY-2001 (first entry)
 T Human mdm2 phosphorothioate oligonucleotide #237.
 X Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 W Homo sapiens.
 X US6184212-B1.
 N 06-FEB-2001.
 D 26-MAR-1999; 99US-0280805.
 F 26-MAR-1998; 98US-0048810.
 R (ISIS-) ISIS PHARM INC.
 A (ISIS-) ISIS PHARM INC.

XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
 PI WPI; 2001-190948/19.
 XX Novel antisense compound 8-30 nucleobases in length targeted to a
 PT nucleic acid molecule encoding human mdm-2 useful for modulating the
 PT expression of human mdm-2 and reducing hyperproliferation of human
 PT cells -
 XX Example 9; Column 31; 77pp; English.
 XX The present invention relates to an antisense compound 8-30
 CC nucleobases in length targeted to nucleobases 1-308 of the
 CC 5' untranslated region, 1776-1806 of the translation termination
 CC codon region or 1818-2370 of the 3' untranslated region of a
 CC nucleic acid molecule encoding human mdm-2. The invention is
 CC useful for reducing hyperproliferation of human cells
 CC modulating the expression of mdm2 in human cells or tissues
 CC or in vitro. The hyperproliferative disorder includes cancer or
 CC psoriasis.
 XX Sequence 20 BP; 9 A; 1 C; 2 G; 8 T; 0 other;
 SQ Query Match 1.0%; Score 12.2; DB 1; Length 20;
 Best Local Similarity 82.4%; Pred. No. 6.2e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1603 AATATGAACATTAA 1619
 Db |||||
 2 AATAAGTTACATTAA 18
 RESULT 870
 AAAL4463/C
 ID AAAL4463 standard; RNA; 21 BP.
 XX AAAL4463;
 AC AAAL4463;
 XX 21-AUG-2000 (first entry)
 DT AUUUA RNA target sequence.
 XX AUUUA sequence; RNA target molecule; RNA binding protein identification;
 KW ss.
 XX Synthetic.
 OS WO200020637-A1.
 XX WO200020637-A1.
 XX 13-APR-2000.
 PD 16-SEP-1999; 99WO-US21672.
 PF 02-OCT-1998; 98US-0165868.
 XX (MESS-) MESSAGE PHARM INC.
 PA Giordano T, Beach DL, Temeles GL;
 PI WPI; 2000-303802/26.
 XX Nucleic acid molecules useful for identifying compounds affecting
 PT interactions between RNA molecules and identifying RNA binding proteins
 PT -
 XX Example 1; Page 33; 58pp; English.
 PS The invention relates to mRNA sequences which bind to RNA binding
 CC proteins, and their use for identifying RNA binding proteins and
 CC compounds which have an effect on the interactions between an RNA
 CC binding protein and an RNA molecule. The disclosed sequences are the 3'
 CC untranslated region (3' UTR) sequences App-R1, App-D3 and App-I1 from

the human amyloid precursor protein mRNA (AA14456-A14458); the 3' UTR of human interleukin-10 (IL-10) mRNA (AA14459); the 3' UTR of human erb-B2 mRNA (AA14460); and the 5' UTR of human insulin-like growth factor I receptor (IGF-IR) mRNA (AA14461). The disclosed mRNA sequences may be used to identify compounds affecting interactions between an RNA molecule comprising the sequence and an RNA binding protein. Such compounds can then be included with a carrier in pharmaceutical compositions for altering expression of a gene comprising the sequences, which can be administered to individuals or cells requiring altered expression of the gene. The mRNA sequences are also useful to identify RNA binding proteins which interact with them. Compounds identified as having the ability to affect such RNA binding interactions may therefore be useful as drugs for modulating protein levels in disease states. The present sequence represents an A14456 RNA sequence used as a target molecule in an exemplification of the invention in an assay for detecting interactions between RNA molecules and RNA binding proteins.

Sequence 21 BP; 6 A; 0 C; 0 G; 15 U; 0 other;

Query Match 1.0%; Score 12.2; DB 1; Length 21;
Best Local Similarity 82.4%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1590 AAATATAAACTAAATA 1606
||||| ||| |||||
20 AAATAAATAAATAAATA 4

SULT 871

D49639/c

AA049639 standard; mRNA; 21 BP.

AA049639;

24-MAR-2003 (first entry)

Human adenylate uridylylate-rich element (ARE) motif mRNA #1.

Amyloidosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer; gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis; autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic; neurodegenerative disorder; Parkinson's disease; gene therapy; virucide; haemostatic; antibacterial; nootropic; neuroprotective; cytostatic; fungicide; human; adenylate uridylylate-rich element; ARE; ss.

Homo sapiens.

WO200283953-A1.

24-OCT-2002.

11-APR-2002; 2002WO-US11757.

11-APR-2001; 2001US-282965P.

(PTCT-) PTC THERAPEUTICS INC.

Rando R, Welch E;

WPI; 2003-075561/07.

Identifying a test compound that binds to a target RNA molecule for treating or preventing amyloidosis, hemophilia, cancer, gigantism, diabetes, by contacting a detectably labeled target RNA molecule with a library of test compounds -

Example; Page 18; 152pp; English.

The invention relates to a method for identifying a test compound that binds to a target RNA molecule, which comprises contacting a detectably labeled target RNA molecule with a library of test compounds under conditions that permit direct binding of the labeled target RNA to a member of the library of test compounds so that a detectably labeled

target RNA-test compound complex is formed. The method is useful for screening libraries of compounds for those that are selectively bind to a pre-selected target RNA. The compounds are useful for inhibiting the formation of a specific bound RNA: host cell factor complexes in vivo. They are also useful for treating or preventing diseases associated with overproduction or decreased protein function, such as amyloidosis, haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism, dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging, inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative disorders, Parkinson's disease or infections (bacterial, viral, fungal). The invention is also used in gene therapy. The present sequence is human adenylate uridylylate-rich element (ARE) motif mRNA. This sequence is used to illustrate the method of the invention.

Sequence 21 BP; 6 A; 0 C; 0 G; 15 U; 0 other;

Query Match 1.0%; Score 12.2; DB 1; Length 21;
Best Local Similarity 82.4%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1590 AAATATAAACTAAATA 1606
||||| ||| |||||
Db 20 AAATAAATAAATAAATA 4

RESULT 872

AA150228/c

ID AA150228 standard; mRNA; 21 BP.

XX AC AA150228;

XX DT 13-FEB-2003 (first entry)

XX DE Human ARE-mRNA sequence #1.

XX KW ARE-mRNA; protein secretion inhibition; ARE-mRNA regulation;

XX KW inflammation; arthritis; autoimmune disease; septic shock; blood clot;

XX KW stroke; TNFalpha; tumor necrosis factor alpha; antiinflammatory;

XX KW antiarthritis; antibacterial; immunosuppressive; cerebroprotective;

XX XX antipyretic; immunomodulator; adenylate-uridylylate rich element; ss.

OS Homo sapiens.

XX PN WO200283842-A2.

XX XX 24-OCT-2002.

XX PF 08-APR-2002; 2002WO-US10898.

XX PR 10-APR-2001; 2001US-282974P.

XX PA (MESS-) MESSAGE PHARM INC.

XX PI Giordano T, Sturgess MA;

XX XX WPI; 2003-046924/04.

XX PT Modulating Adenylate-Uridylate Rich element-mRNA regulation involves administering new amide compound that inhibits secretion of protein encoded by ARE-mRNA, useful for treating inflammation, arthritis and autoimmune diseases -

XX PS Disclosure; Fig 5; 147pp; English.

XX CC The present invention relates to a method of modulating the regulation of an adenylate-uridylylate rich element (ARE)-mRNA, which involves administering new compounds that inhibits secretion of a protein encoded by an ARE-mRNA. This can be used in the treatment of inflammation, arthritis, autoimmune diseases, septic shock, blood clot, stroke, fever, acute respiratory distress syndrome (ARDS) and cachexia. The present sequence is an ARE-mRNA shown in the exemplification of the invention.

XX SQ Sequence 21 BP; 6 A; 0 C; 0 G; 1 T; 14 U; 0 other;

Query Match 1.0%; Score 12.2; DB 1; Length 21;
 Best Local Similarity 82.4%; Pred. No. 6.3e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 1590 AAATATAAAGTAATA 1606
 b 20 AAATAAATAAATAAATA 4
 ||||| ||||| |||||

RESULT 873
 AA53707/C
 D AAL53707 standard; RNA; 21 BP.
 X
 C AAL53707;
 X
 T 07-FEB-2003 (first entry)
 X
 E Adenylate Uridylate-rich element motif SEQ ID No 1.
 X
 W Target RNA; target RNA:support-attached test compound; flow cytometry;
 N mass spectrometry; high-throughput screening; RNA motif; ss.
 X
 S Homo sapiens.
 X
 N WC200283837-A1.
 X
 D 24-OCT-2002.
 X
 F 11-APR-2002; 2002WO-US11758.
 X
 R 11-APR-2001; 2001US-282966P.
 X
 A (PTCT-) PTC THERAPEUTICS INC.
 X
 I Almstead NG;
 X
 R WPI; 2003-075534/07.
 X
 C Identifying a test compound that binds to a target RNA molecule by
 PT separating the detectably labeled target RNA:support-attached test
 PT compound complex from uncomplexed target RNA molecules and test
 PT compounds by flow cytometry -
 X
 S Disclosure; Page 16; 131pp; English.

The invention relates to a novel method for identifying a test compound
 CC that binds to a target RNA molecule comprising separating the detectably
 CC labeled target RNA:support-attached test compound complex from
 CC uncomplexed target RNA molecules and test compounds. The separating
 CC process is carried out by flow cytometry and determining a structure of
 CC the type of test compound of the RNA:support-attached test compound
 CC complex by mass spectrometry. The method is useful for high-throughput
 CC screening of libraries of compounds to identify pharmaceutical leads.
 CC This polynucleotide sequence represents one of the target RNA motifs/
 CC regions of the invention.

Sequence 21 BP; 6 A; 0 C; 0 G; 15 U; 0 other;

Query Match 1.0%; Score 12.2; DB 1; Length 21;
 Best Local Similarity 82.4%; Pred. No. 6.3e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 1590 AAATATAAAGTAATA 1606
 b 20 AAATAAATAAATAAATA 4
 ||||| ||||| |||||

RESULT 874
 AA58890
 ID AAV58890 standard; DNA; 17 BP.
 X
 X AAV58890;
 AC

XX 20-JAN-1999 (first entry)
 DT
 XX Primer C5 for Cytochrome C551 I coding sequence.
 DE
 XX Cytochrome C551; vitamin C production; electron transfer mediator;
 KW aldehyde production; ketone production; carboxylic acid production;
 KW alcohol dehydrogenase; aldehyde dehydrogenase; PCR primer; ss.
 XX
 OS Synthetic.
 OS Gluconobacter oxydans.
 XX
 XX EP869175-A2.
 PN
 XX 07-OCT-1998.
 PD
 XX 27-MAR-1998; 98EP-0105608.
 PF
 XX 04-APR-1997; 97EP-0105583.
 PR
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA
 XX Asakura A, Hoshino T, Shinjoh M, Tomiyama N;
 PI WPI; 1998-508491/44.
 DR
 XX New Gluconobacter cytochrome c551 polypeptides I and II - useful as
 PT electron transfer mediators and especially for producing vitamin C
 PS
 XX Example 2; Fig 2; 22pp; English.

This sequence is a primer for DNA encoding the Gluconobacter cytochrome
 CC C551 I of the invention. The cytochrome C551 I protein has: (a) a
 CC molecular weight of 17-20kDa; (b) an absorption spectrum (for reduced
 CC form) with alpha, beta and gamma peaks at 551, 522 and 417 nm
 CC respectively; (c) a haem content of about 1 mole/mole protein; and (d) an
 CC isoelectric point of about 3.95. The novel cytochrome c is especially
 CC useful for producing vitamin C, as it is an electron transfer mediator
 CC which improves production of aldehydes, ketones and carboxylic acids from
 CC corresponding substrates in the presence of alcohol dehydrogenase and
 CC aldehyde dehydrogenase enzymes (ADH). It especially improves production
 CC of 2-KGA (an intermediate of vitamin C) from L-sorbose or D-sorbose. It
 CC can also be used as a source for protein-protein conjugates such as
 CC ADH-cytochrome c551 to improve total electron transfer efficiency.

Sequence 17 BP; 8 A; 1 C; 1 G; 2 T; 5 other;

Query Match 1.0%; Score 12; DB 1; Length 17;
 Best Local Similarity 71.4%; Pred. No. 6e+02;
 Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1250 ATAAACACACATA 1263
 ||:||||:||||:
 Db 1 ATAAAYAAAYATA 14

RESULT 875
 AAV58891/C
 ID AAV58891 standard; DNA; 17 BP.
 XX
 AC AAV58891;
 XX
 DT 20-JAN-1999 (first entry)
 XX
 XX Primer CSR for Cytochrome C551 I coding sequence.
 DE
 XX Cytochrome C551; vitamin C production; electron transfer mediator;
 KW aldehyde production; ketone production; carboxylic acid production;
 KW alcohol dehydrogenase; aldehyde dehydrogenase; PCR primer; ss.
 XX
 OS Synthetic.
 OS Gluconobacter oxydans.
 XX

PA (NYEE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

XX Crow MK, Li Y;

XX WPI; 2001-244776/25.

XX New altered CD40L promoter for use in the study, diagnosis and
PT treatment of a variety of inflammatory disorders and autoimmune
PT diseases, such as rheumatoid arthritis -

XX Example 1; Fig 2; 90pp; English.

XX The present invention describes an isolated, purified nucleic acid,
XX which is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand,
XX having residues 331-455 of the sequence comprising 455 nucleotides given
XX in AAF74905 where A in the wild type sequence at position 331
XX (corresponding to position -125) is replaced with C. (I) has
XX antiarthritic, antirheumatic, immunosuppressive and antiinflammatory
XX activities, and can be used in gene therapy. (I) is useful in the study,
XX diagnosis and treatment of inflammatory and autoimmune diseases, as well
XX as diseases in which elevated expression of CD40L is a factor,
XX e.g., rheumatoid arthritis. The present sequence represents a PCR primer
XX for the human CD40L promoter sequence, which is used in an example from
XX the present invention.

XX Sequence 21 BP; 5 A; 4 C; 2 G; 10 T; 0 other;

XX Query Match 1.0%; Score 12; DB 1; Length 21;

XX Best Local Similarity 75.0%; Pred. No. 6.8e+02;

XX Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

XX 1251 TAAACAAACAAATATTTT 1270

XX 20 TAAAGAGAGAACAGTTCT 1

XX RESULT 878

XX AAT55794/C

XX AAT556318 standard; RNA; 15 BP.

XX AAT556318;

XX 25-MAR-2003 (updated)

XX 14-MAY-1997 (first entry)

XX Mouse TNF-a hammerhead ribozyme target sequence (nt position 1308).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
XX intercellular adhesion molecule; rel A; tumour necrosis factor;
XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
XX translocation; chronic myelogenous leukaemia; CML; cancer;
XX Philadelphia chromosome; inflammation; autoimmune disease;
XX atherosclerosis; myocardial infarction; stroke; restenosis;
XX transplant rejection; rheumatoid arthritis; psoriasis;
XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;
XX human immunodeficiency virus; acquired immune deficiency syndrome;
XX AIDS; ss.

XX Mus musculus.

XX W09523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-IB00156.

XX 30-JAN-1995; 95US-0380734.

XX 23-FEB-1994; 94US-0201109.

XX 29-MAR-1994; 94US-0218934.

XX 04-APR-1994; 94US-0222795.

XX 07-APR-1994; 94US-0224483.

XX 15-APR-1994; 94US-0227958.

PR 15-APR-1994; 94US-0228041.
PR 18-MAY-1994; 94US-0245716.
PR 06-JUL-1994; 94US-0271280.
PR 15-AUG-1994; 94US-0291932.
PR 16-AUG-1994; 94US-0291433.
PR 17-AUG-1994; 94US-0292620.
PR 19-AUG-1994; 94US-0293520.
PR 02-SEP-1994; 94US-0300000.
PR 08-SEP-1994; 94US-0303039.
PR 23-SEP-1994; 94US-0311486.
PR 23-SEP-1994; 94US-0311749.
PR 28-SEP-1994; 94US-0314397.
PR 03-OCT-1994; 94US-0316771.
PR 07-OCT-1994; 94US-0319492.
PR 11-OCT-1994; 94US-0321993.
PR 04-NOV-1994; 94US-0334847.
PR 10-NOV-1994; 94US-0337608.
PR 28-NOV-1994; 94US-0345516.
PR 16-DEC-1994; 94US-0357577.
PR 23-DEC-1994; 94US-0363233.
XX (RIBO-) RIBOZYME PHARM INC.

XX Stinchcomb DT, Chowrira B, Dizenzo A, Draper KG, Dudycz LW;

PI Griem S, Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;

PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;

PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;

XX WPI; 1995-351090/45.

XX Ribozymes having modified bases and methods for producing them -

XX for use in inhibiting disease related genes

XX Claim 2; Page 252; 407pp; English.

XX The present sequence represents a preferred target sequence for an

XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha

XX mRNA at the nucleotide base position indicated in the D3 line.

XX Regions of the mRNA that do not form secondary folding

XX structures and that contain potential hammerhead and hairpin

XX ribozyme cleavage sites were identified by computer analysis.

XX Ribozymes directed against these mRNA sequences were designed and

XX synthesised with modifications that improve their nuclease

XX resistance. The ribozymes are designed to cleave the target

XX sequences and thereby inhibit TNF-alpha expression, making them

XX potentially useful for treating rheumatoid arthritis, septic shock

XX and other inflammatory disorders including psoriasis, as well as

XX for treatment of AIDS.

XX (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 15 BP; 5 A; 0 C; 0 G; 10 U; 0 other;

XX SQ

XX Query Match 0.9%; Score 11.8; DB 1; Length 15;

XX Best Local Similarity 86.7%; Pred. No. 5.9e+02;

XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 1251 TAAACAAACAAATAT 1265

XX 15 TAAATATATATATAT 1

XX RESULT 879

XX AAT55794/C

XX ID AAT55794 standard; RNA; 15 BP.

XX AAT55794;

XX 25-MAR-2003 (updated)

XX 25-MAR-1997 (first entry)

XX Human TNF-alpha hammerhead ribozyme target sequence (nt position 1256).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;

Gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
intercellular adhesion molecule; rel A; tumour necrosis factor;
TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
translocation; chronic myelogenous leukaemia; CML; cancer;
Philadelphia chromosome; inflammation; autoimmune disease;
atherosclerosis; myocardial infarction; stroke; restenosis;
transplant rejection; rheumatoid arthritis; psoriasis;
myocardial ischaemia; Kawasaki disease; septic shock; HIV;
human immunodeficiency virus; acquired immune deficiency syndrome;
AIDS; ss.

Homo sapiens.

W09523225-A2.

31-AUG-1995.

23-FEB-1995; 95WO-IB00156.

30-JAN-1995; 95US-0380734.

23-FEB-1994; 94US-0201109.

29-MAR-1994; 94US-0218934.

04-APR-1994; 94US-0222795.

07-APR-1994; 94US-0224483.

15-APR-1994; 94US-0227958.

15-APR-1994; 94US-0228041.

18-MAY-1994; 94US-0245736.

06-JUL-1994; 94US-0271280.

15-AUG-1994; 94US-0291932.

16-AUG-1994; 94US-0291433.

17-AUG-1994; 94US-0292620.

19-AUG-1994; 94US-0293520.

02-SEP-1994; 94US-0300000.

08-SEP-1994; 94US-0303039.

23-SEP-1994; 94US-0311486.

23-SEP-1994; 94US-0311749.

28-SEP-1994; 94US-0314397.

03-OCT-1994; 94US-0316771.

07-OCT-1994; 94US-0319492.

11-OCT-1994; 94US-0321993.

04-NOV-1994; 94US-0334847.

10-NOV-1994; 94US-0337608.

28-NOV-1994; 94US-0345516.

16-DEC-1994; 94US-0357577.

23-DEC-1994; 94US-0363233.

(RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Chowira B, Drenzo A, Draper KG, Dudycz LW;
Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
Modak A, Pavco P, Seigleman L, Sullivan SM, Sweedler D;
Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;

WPI; 1995-351090/45.

Ribozymes having modified bases and methods for producing them -
for use in inhibiting disease related genes

Claim 2; Page 242; 407pp; English.

The present sequence represents a preferred target sequence for an
enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
mRNA at the nucleotide base position indicated in the DE line.
Regions of the mRNA that do not form secondary folding
structures and that contain potential hammerhead and hairpin
ribozyme cleavage sites were identified by computer analysis.
Ribozymes directed against these mRNA sequences were designed and
synthesised with modifications that improve their nuclease
resistance. The ribozymes are designed to cleave the target
sequences and thereby inhibit TNF-alpha expression, making them
potentially useful for treating rheumatoid arthritis, septic shock
and other inflammatory disorders including psoriasis, as well as
for treatment of AIDS.

CC (Updated on 25-MAR-2003 to correct PI field.)
XX Sequence 15 BP; 5 A; 0 C; 0 G; 10 U; 0 other;
SQ

Query Match 0.9%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 5.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 TAAACACACAAATAAT 1265

DB 15 TAAATAATATAATAAT 1

RESULT 880

AAQ92084/c

ID AAQ92084 standard; cDNA; 17 BP.

XX AAQ92084;

XX AAQ92084;

DT 25-MAR-2003 (updated)

DT 07-JAN-1996 (first entry)

DE Renilla reniformis luciferase DNA probe-1.

KW Luciferase; enzyme; bioluminescence; luminescence; label; DNA probe;
KW antibody; oligonucleotide; ss.
XX Synthetic.

XX US5418155-A.

XX 23-MAY-1995.

PF 14-DEC-1993; 93US-0167650.

PR 29-DEC-1989; 89US-0458952.

PR 20-AUG-1992; 92US-0933017.

PR 17-JUN-1993; 93US-0079700.

PR 14-DEC-1993; 93US-0167650.

XX (UYGE-) UNIV GEORGIA RES FOUND INC.

XX Cormier MJ, Lorenz WW;

XX WPI; 1995-199741/26.

XX New recombinant Renilla luciferase polypeptide - used as a
luminescent tag, partic in bio-luminescence assays and for the prodn
of antibodies
XX Disclosure; Fig. 4; 18pp; English.
XX This 17-mer oligonucleotide DNA probe, along with Probe-2 (AAQ92085)
are used to screen an R. reniformis cDNA library to isolate cDNA
encoding Renilla luciferase. The luciferase was then expressed
using E. coli.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX (Updated on 25-MAR-2003 to correct DR field.)
XX Sequence 17 BP; 6 A; 0 C; 2 G; 9 T; 0 other;

Query Match 0.9%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1005 ACATAAATTTTTC 1019

DB 15 AAAAAAATTTTTC 1

RESULT 881

AAF02054

ID AAF02054 standard; DNA; 17 BP.

AC ANF02054;
 DT 16-FEB-2001 (first entry)
 DE Hammerhead ribozyme substrate #349.
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 W interferon alpha; ss.
 X Homo sapiens.
 N WO2000061729-A2.
 D 19-OCT-2000.
 X 11-APR-2000; 2000WO-US09721.
 R 12-APR-1999; 99US-0129390.
 A (RIBO-) RIBOZYME PHARM INC.
 I Blatt L, Zwick M, Pavco P, McSwiggen J;
 R WPI; 2000-647423/62.
 T Enzymatic and antisense nucleic acid inhibition of repressor genes,
 T useful for producing e.g. granulocyte colony stimulating factor
 T protein, interferon alpha and erythropoietin -
 X Claim 37; Page 63; 164pp; English.
 C The present invention relates to enzymatic and antisense nucleic acid
 C molecules that act as inhibitors of the expression of repressor genes
 C encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 C transcription factor gene, Irf-2 and/or the C/EBP Displacement
 C Protein (CBP). Inhibition of the repressors removes prevents
 C inhibition (and consequently increases expression of) genes involved in
 C the production of erythropoietin, granulocyte colony stimulating factor
 C protein and interferon alpha.
 X Sequence 17 BP; 7 A; 1 C; 1 G; 8 T; 0 other;
 Q
 Query Match 0.9%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 6.5e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Y 1004 AACATAAATTTATTTT 1018
 b | | | | | | | | | | | | | | | |
 1 AAATAAATTTATTTT 15
 RESULT 882
 BT39376/C
 D ABT39376 standard; DNA; 17 BP.
 X
 C ABT39376;
 X
 T 12-JUN-2003 (first entry)
 E Tumour suppression related human fukutin oligo SEQ ID No 5013.
 X
 X Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 W antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 W schizophrenia; protein chip; gene therapy; tumour suppression;
 W human fukutin; ds.
 X Homo sapiens.
 S
 X WO2003025175-A2.
 X
 N 27-MAR-2003.
 D

PF 17-SEP-2002; 2002WO-IB04208.
 XX
 PR 17-SEP-2001; 2001FR-0011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 FI Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 DR
 XX
 XX New isolated nucleic acid, useful for treating viral diseases
 PT associated with tumors and cell degeneration, also related
 PT polypeptides, antibodies and transfected cells -
 FI Disclosure; Page 620; 720pp; French.
 PS
 XX
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15
 CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
 CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
 CC sequence that hybridizes to them under highly stringent conditions, or
 CC the complement of any of them, or the corresponding RNA. The novel
 CC isolated nucleic acids of the invention are useful as probes and primers
 CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
 CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
 CC and for production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention.
 XX
 SQ Sequence 17 BP; 9 A; 4 C; 1 G; 3 T; 0 other;
 Query Match 0.9%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 6.5e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1286 TTGTTTATCTGAAT 1300
 Db | | | | | | | | | | | | | | | |
 16 TTGTTTATCTGAGT 2
 RESULT 883
 ABZ60265
 ID ABZ60265 standard; RNA; 17 BP.
 XX
 AC ABZ60265;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human K-Ras DNazyme substrate #377.
 XX
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 XX anti-rheumatic; cancer; AIDS; ss.
 OS Homo sapiens.
 XX
 XX WO200297114-A2.
 PN
 XX
 PD 05-DEC-2002.
 XX
 XX 29-MAY-2002; 2002WO-US16840.
 PF
 XX 29-MAY-2001; 2001US-294140P.
 PR

Claim 18; Page 118; 164pp; English.

The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute

lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferation disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients.

Sequence 18 BP; 3 A; 1 C; 4 G; 10 T; 0 other;

Query Match 0.9%; Score 11.8; DB 1; Length 18;

Best Local Similarity 86.7%; Pred. No. 6.7e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1243 ATTTCAGTAACAA 1257

|||||
15 ATTTCGAAACAA 1

RESULT 886

AAV82030

ID AAV82030 standard; DNA; 18 BP.

XX AC AAV82030;

XX 21-JUN-1999 (first entry)

XX Moraxella lactoferrin binding protein 1 (lbpl) PCR primer.

XX Lactoferrin receptor; lactoferrin binding protein; lbpl;

XX lbpA gene; infection; otitis media; sinusitis; conjunctivitis;

XX pneumonia; bronchitis; tracheitis; emphysema; diagnosis; therapy;

XX vaccine; Branhamella catarrhalis; PCR; primer; ss.

XX Synthetic.

XX Moraxella catarrhalis.

XX WO9855606-A2.

XX 10-DEC-1998.

XX 02-JUN-1998; 98WO-CA00544.

XX 08-MAY-1998; 98US-0074658.

XX 03-JUN-1997; 97US-0867941.

XX (CONN-) CONNAUGHT LAB LTD.

XX Du R, Klein MH, Loosmore SM, Wang Q, Yang Y;

XX WPI; 1999-070266/06.

XX Lactoferrin receptor genes from Moraxella, especially M. catarrhalis

XX - useful to diagnose Moraxella infection e.g. to detect otitis media

XX due to M. catarrhalis infection and to immunise against such

XX infections

XX Example 1; Page 37; 202pp; English.

XX This PCR primer is based on a C-terminal peptide (see AAV89423) of

XX Moraxella catarrhalis lactoferrin binding protein 1 (lbpl). PCR

XX primers (see AAV82030-31) based on this C-terminal peptide and other

XX primers (see AAV82022-29) based on an isolated N-terminal peptide,

XX are used in the amplification of M. catarrhalis lbpA genes that

XX code for lbpl. The invention provides immunogenic compositions,

XX including vaccines, based upon expressed recombinant lbpl and/or

XX lbp2 and/or ORF3 proteins (see AAV89413-21) for use in the prevention

XX of diseases (e.g. otitis media) caused by Moraxella. The genes and

XX DNA sequences of the Moraxella lactoferrin receptor (lfr) locus

CC (see AAV82019-21) are useful for diagnosis, immunisation, and the

CC generation of diagnostic and immunological reagents.

XX Sequence 18 BP; 7 A; 1 C; 3 G; 7 T; 0 other;

XX Query Match 0.9%; Score 11.8; DB 1; Length 18;

XX Best Local Similarity 86.7%; Pred. No. 6.7e+02;

XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1161 TTAATGATGTTTAA 1175

|||||

3 TGAATGAAGTTTAA 17

DB

RESULT 897

AAV82031/C

ID AAV82031 standard; DNA; 18 BP.

XX AC AAV82031;

XX 21-JUN-1999 (first entry)

XX Moraxella lactoferrin binding protein 1 (lbpl) PCR primer.

XX Lactoferrin receptor; lactoferrin binding protein; lbpl;

XX lbpA gene; infection; otitis media; sinusitis; conjunctivitis;

XX pneumonia; bronchitis; tracheitis; emphysema; diagnosis; therapy;

XX vaccine; Branhamella catarrhalis; PCR; primer; ss.

XX Synthetic.

XX Moraxella catarrhalis.

XX WO9855606-A2.

XX 10-DEC-1998.

XX 02-JUN-1998; 98WO-CA00544.

XX 08-MAY-1998; 98US-0074658.

XX 03-JUN-1997; 97US-0867941.

XX (CONN-) CONNAUGHT LAB LTD.

XX Du R, Klein MH, Loosmore SM, Wang Q, Yang Y;

XX WPI; 1999-070266/06.

XX Lactoferrin receptor genes from Moraxella, especially M. catarrhalis

XX - useful to diagnose Moraxella infection e.g. to detect otitis media

XX due to M. catarrhalis infection and to immunise against such

XX infections

XX Example 1; Page 37; 202pp; English.

XX This PCR primer is based on a C-terminal peptide (see AAV89423) of

XX Moraxella catarrhalis lactoferrin binding protein 1 (lbpl). PCR

XX primers (see AAV82030-31) based on this C-terminal peptide and other

XX primers (see AAV82022-29) based on an isolated N-terminal peptide,

XX are used in the amplification of M. catarrhalis lbpA genes that

XX code for lbpl. The invention provides immunogenic compositions,

XX including vaccines, based upon expressed recombinant lbpl and/or

XX lbp2 and/or ORF3 proteins (see AAV89413-21) for use in the prevention

XX of diseases (e.g. otitis media) caused by Moraxella. The genes and

XX DNA sequences of the Moraxella lactoferrin receptor (lfr) locus

XX generation of diagnostic and immunological reagents.

XX Sequence 18 BP; 7 A; 3 C; 1 G; 7 T; 0 other;

XX Query Match 0.9%; Score 11.8; DB 1; Length 18;

XX Best Local Similarity 86.7%; Pred. No. 6.7e+02;

XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1161 TTAATGATGTTTAA 1175
D 16 TGAATGAGTTTAA 2

RESULT 888

AH56758

AAH56758 standard; DNA; 19 BP.

AAH56758;

06-SEP-2001 (first entry)

S. aureus groE operon antisense oligonucleotide SEQ ID NO:406.

Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth; microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis; Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa; antibacterial; antiviral; antiproliferative; antisense therapy; microbial infection; ss.

Staphylococcus aureus.

WO200136625-A2.

25-MAY-2001.

20-NOV-2000; 2000WO-CA01347.

18-NOV-1999; 99US-0166249.

(GENE-) GENESENSE TECHNOLOGIES INC.

Wright JA, Young AH, Dugourd D;

WPI; 2001-355633/37.

Novel antisense compounds targeting nucleic acid encoding groEL or groES gene of microorganism, which hybridize with and inhibit expression of the genes, useful to inhibit growth of microorganism having the genes -

Claim 3; Page 52; 110pp; English.

The present invention specifically claims AAH56368 to AAH56832 which are antisense oligonucleotides to nucleotide sequences encoding groE. More generally, antisense compounds (I) comprising antisense oligonucleotides of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a microorganism, where the antisense compound is complementary to GL or GS of a microorganism and specifically hybridizes with and inhibits the expression of GL or GS, is claimed. (I) have antibacterial, antiviral and antiproliferative activities, and can be used in antisense therapy and for inhibition of expression of groES or groEL. (I) are useful for inhibiting expression of GL or GS in cells or tissues in vitro. (I) are also useful for inhibiting the growth of a microorganism, or inhibiting the expression of GL or GS gene in a microorganism (a bacterial cell or a virus) having a GL or GS gene which involves administering to the microorganism or to a cell infected with the microorganism, (I). (I) are also useful for treating a mammalian pathological condition mediated by the microorganisms which involves identifying a eukaryotic organism having a pathological condition mediated by microorganisms having a GL or GS gene and administering (I) such that the growth of microorganism is inhibited. The antisense compounds are utilised for diagnostics, therapeutics, prophylaxis and as research reagents and kits, e.g., to prevent or delay microbial infections in humans. They are also useful as molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854 represent PCR primers for groE sequences which are used in the exemplification of the present invention. AAH56855 to AAH56870 represent groE nucleotide sequence given in the present invention.

Sequence 19 BP; 6 A; 1 C; 0 G; 12 T; 0 other;

Query Match 0.9%; Score 11.8; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. NO. 7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1139 TAAATTTATTTTATT 1153

DB 4 TAAATTTATTTTATT 18

RESULT 889

AAH76783

ID AAH76783 standard; DNA; 24 BP.

AC AAH76783;

XX 14-DEC-2001 (first entry)

XX Human nuclear transforming protein 13 RT-PCR primer, SEQ ID NO:4.

KW Human; nuclear transforming protein 13; ATP/GTP binding domain;
KW recombinant production; malignant tumour; cancer; blood disease;
KW HIV infection; human immunodeficiency virus; immune disorder;
KW inflammatory condition; cytostatic; anti-HIV; antiinflammatory;
KW immunomodulator; reverse transcription-PCR; RT-PCR primer; ss.

XX Homo sapiens.

XX WO200172800-A1.

XX 04-OCT-2001.

XX 26-MAR-2001; 2001WO-CN00437.

XX 27-MAR-2000; 2000CN-0115183.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX Mao Y, Xie Y;

XX WPI; 2001-597103/67.

PT Human nuclear transforming protein 13 containing ATP/GTP binding domain
PT and encoded polynucleotide, applicable in diagnosis and treatment of
PT malignant neoplasm, hemopathy, HIV infection, immunological diseases
PT and inflammations -

Example 2; Page 18; 37pp; Chinese.

XX The invention relates to human nuclear transforming protein 13
CC (AAG56744), nucleic acids encoding it (AAH76781), and a method for the
CC recombinant production of nuclear transforming protein 13. The protein
CC contains an ATP/GTP binding domain and has a molecular weight of 13 kD.
CC The present invention additionally discloses an antagonist of nuclear
CC transforming protein 13 for therapeutic use, and an antibody which
CC specifically binds to human nuclear transforming protein 13. Nuclear
CC transforming protein 13, and nucleotides which encode it may be used
CC for treating a variety of diseases, such as malignant tumours, blood
CC diseases, HIV (human immunodeficiency virus) infection, immune disorders
CC modulators of its activity or for peptide fingerprinting identification.
CC The polynucleotide can be used as a primer for nucleic acid amplification.
CC reactions or as a probe for hybridisation reactions, or in producing gene
CC chips or microarrays. Sequences AAH76782-AAH76783 represent reverse
CC transcription-PCR (RT-PCR) primers used in an exemplification of the
CC invention to isolate human nuclear transforming protein 13 cDNA.

SQ Sequence 24 BP; 6 A; 4 C; 1 G; 13 T; 0 other;

Query Match 0.9%; Score 11.8; DB 1; Length 24;

Best Local Similarity 69.8%; Pred. NO. 7.6e+02;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1133 TTATAGTAATTTATTTTATT 1155

b 1 TCTTGCACAAATATTATTTCT 23

RESULT 890
AH45430/c
D AAH45430 standard; DNA; 25-BP.
C X
C AAH45430;
X T
T 06-SEP-2001 (first entry)
E X Glutamate tRNA synthetase 58 cDNA specific PCR primer.
E Human; glutamate tRNA synthetase 58; malignant tumour; haemopathy;
W HIV infection; immunological disease; inflammatory condition; cytostatic;
W haemostatic; virucide; immunomodulatory; antiinflammatory,
W PCR primer; ss.
X S Homo sapiens.
S X WO200138371-A1.
N N 31-MAY-2001.
D X
X P 20-NOV-2000; 2000WO-CN00475.
F X
R 24-NOV-1999; 99CN-0124102.
X X (BIOR-) BIORAD GENE DEV LTD SHANGHAI.
I I Mao Y, Xie Y;
I WPI; 2001-355891/37.
R X
Y New human glutamate tRNA synthase 58 for diagnosing and treating
T cancer, hemopathy, human immunodeficiency virus (HIV) infection,
T immunological diseases and inflammation
X Example 3; Page 12; 36pp; Chinese.

X This invention relates to human glutamate tRNA synthetase 58, and the
X cDNA sequence encoding it. The invention includes a vector containing the
X cDNA sequence, a host cell transformed with the vector, and an antibody
X targeting the glutamate tRNA synthetase 58 protein. The glutamate tRNA
X synthetase 58 protein and cDNA may be used in the diagnosis and treatment
X of malignant tumors, haemopathy; human immunodeficiency virus (HIV)
X infection, immunological diseases and various inflammatory conditions.
X Use of the protein or cDNA for treatment, may result in cytostatic;
X haemostatic; virucide; immunomodulatory; or antiinflammatory activity.
X The present sequence represents a PCR primer specific for cDNA encoding
X human glutamate tRNA synthetase 58.

X Sequence 25 BP; 5 A; 1 C; 0 G; 19 T; 0 other;

Query Match 0.9%; Score 11.8; DB 1; Length 25;
Best Local Similarity 69.6%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0.

Dy 1604 ATRTGMAACATTTAAAAATAAAT 1626
||| ||| ||| ||| ||| ||| |||
Db 25 AAAATAAATAAATAAATAAAT 3

RESULT 891
AAAL51650/c
IID AAAL51650 standard; DNA; 38 BP.
ID AC
XX AAAL51650;
XX
XT 17-APR-2003 (first entry)
XD Interleukin 8 capture probe.
XE

Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
restenosis; ss.

Mammalia.

WO200032765-A2.

08-JUN-2000.

06-DEC-1999; 99WO-US28772.

04-DEC-1998; 98US-0110954.

(IMMU-) IMMUSOL INC.

Tritz R, Welch PJ, Barber JR, Robbins JM;

WPI; 2000-412314/35.

New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1 -

Example 1; Page 18; 109pp; English.

The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AA82415 to AA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment.

Sequence 18 BP; 7 A; 2 C; 2 G; 7 T; 0 other;

Query Match 0.9%; Score 11.6; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 7.3e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

830 GGATTTTTCCTGTTAA 847
||| ||| ||| ||| |||
1 GGAAATTTCTCTATTAA 18

SULT 893

H61772

AAH61772 standard; DNA; 18 BP.

AAH61772;

10-SEP-2001 (first entry)

Cdc 2 kinase hammerhead ribozyme recognition site SEQ ID NO:4196.

Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnery; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antiproliferative; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keratolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss.

Homo sapiens.
Synthetic.

WO200130362-A2.

03-MAY-2001.

PF XX 26-OCT-2000; 2000WO-US29500.
PR XX 26-OCT-1999; 99US-0161532.
XX XX (IMMU-) IMMUSOL INC.
PA XX Robbins JM, Tritz R;
PI XX WPI; 2001-300427/31.
DR XX
XX XX
PT XX Treating proliferative skin or eye diseases and scarring, using
PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
PT matrix metalloproteinases, growth factors and cell-cycle dependent
PT kinases -
XX XX
PS XX
XX XX
XX XX
XX XX
CC XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antiproliferative,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnery, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative
CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention.
XX XX
SQ Sequence 18 BP; 7 A; 2 C; 2 G; 7 T; 0 other;

Query Match 0.9%; Score 11.6; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 7.3e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 830 GGATTTTTCCTGTTAA 847
||| ||| ||| ||| |||
DB 1 GGAAATTTCTCTATTAA 18

RESULT 894

ABZ11062

ID ABZ11062 standard; DNA; 18 BP.

AC ABZ11062;

DT 16-JAN-2003 (first entry)

Haematopoietic cell proliferation disorder related oligonucleotide #1202.

Human; haematopoietic cell proliferation disorder; cytostatic;
gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
cytosine methylation state; probe; primer; ss.

Homo sapiens.
OS Synthetic.

WO20027272-A2.

PD 03-OCT-2002.

XX 26-MAR-2002; 2002WO-EP03401.

PR 26-MAR-2001; 2001US-278333P.

A (EPIC-) EPIGENOMICS AG.
I Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
I Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
I Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T;
I Pelet C, Schwepe I, Ziebarth H;
R WPI; 2003-018942/01.
K
R
S
I Detecting and differentiating between hematopoietic cell proliferative
I disorders, comprises contacting a target nucleic acid with a reagent
I that distinguishes between methylated and non-methylated CpG
I dinucleotides -
K
S Claim 15; Page 78; 117pp; English.
C The present invention describes a method for detecting and
C differentiating between hematopoietic cell proliferative disorders
C associated with at least 1 gene and/or their regulatory regions in a
C subject. The method comprises contacting a target nucleic acid in a
C biological sample obtained from the subject with at least 1 reagent,
C which distinguishes between methylated and non-methylated CpG
C dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
C represent specifically claimed nucleotide sequences from the present
C invention. Oligonucleotides from the present invention can be used for
C differentiating between healthy hematopoietic cells and proliferative
C disorder hematopoietic cells; for differentiating between acute
C lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
C determining the cytosine methylation state and/or single nucleotide
C polymorphisms (SNPs) of hematopoietic cell proliferation disorder
C related sequences and their complements; and as primers for the
C amplification of hematopoietic cell proliferation disorder related
C DNA sequences. The nucleotide sequences from the present invention can
C also be used for detecting a predisposition to, differentiation between
C subclasses, diagnosis, prognosis, treatment and/or monitoring of
C hematopoietic cell proliferative disorders. The present method enables
C a highly specific classification of hematopoietic cell proliferative
C disorders allowing for improved and informed treatment of patients.
X
Q Sequence 18 BP; 4 A; 0 C; 3 G; 11 T; 0 other;
Query Match 0.9%; Score 11.6; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 7.3e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
NY 1263 AATTTTGTAGTAAGTA 1280
yb 1 AATTTTGTAGTAAGTA 18
RESULT 895
AA62676/c
ID AAA62676 standard; DNA; 19 BP.
AC AAA62676;
AT 08-JAN-2001 (first entry)
DE Cry2A family gene shuffling PCR primer 1 for.
CX Cry2Aa; Cry2Ab; Cry2Ac; family gene shuffling; recombinant;
KW nucleic acid diversity; mutagen synthesis; PCR primer; ss.
CX Unidentified.
CX WO200042561-A2.
PN 20-JUL-2000.
CX 18-JAN-2000; 2000WO-US01203.
CX 19-JAN-1999; 99US-0116447.
PR 05-FEB-1999; 99US-0118813.
PR

PR 05-FEB-1999; 99US-0118854.
PR 24-JUN-1999; 99US-0141049.
PR 28-SEP-1999; 99US-0408392.
PR 28-SEP-1999; 99US-0408393.
PR 12-OCT-1999; 99US-0418375.
PR 12-OCT-1999; 99US-0418637.
XX
XX (MAXY-) MAXYGEN INC.
XX
XX Cramer A, Stemmer WPC, Minshull J, Bass SH, Welch M, Ness JE;
PI Gustafsson C, Patten PA;
XX WPI; 2000-482862/42.
DR
XX
XX Recombining homologous nucleic acids to produce family shuffle nucleic
FT acids comprises hybridizing and elongating a set of family gene
FT shuffling oligonucleotides and providing a population of recombined
FT nucleic acids -
XX
XX Example; Page 54; 74pp; English.
XX
CC The present sequence is a PCR primer used in a method for shuffling genes
CC cry2Aa, cry2Ab and cry2Ac. Gene shuffling is a process for
CC generating recombinant nucleic acids. Oligonucleotide assisted
CC approaches can be used to produce family shuffled nucleic acids without
CC isolating or cloning full-length homologous nucleic acids. Family gene
CC shuffling oligonucleotides are provided by aligning homologous nucleic
CC acid sequences to select conserved regions of sequence identity and
CC regions of sequence diversity. A plurality of oligonucleotides are
CC synthesized which correspond to at least one region of sequence
CC diversity. In this example, the oligonucleotides were spiked into
CC the assembling mix and PCR was then performed using the present primer.
CC The method can be used to produce a family of shuffled nucleic acids, to
CC produce recombinant molecules with greater molecular diversity and to
CC generate classical mutagens. Homologous nucleic acids with low sequence
CC similarity and non-homologous nucleic acids are also easily recombined.
XX
SQ Sequence 19 BP; 9 A; 0 C; 3 G; 7 T; 0 other;
Query Match 0.9%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 7.5e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 501 ATGCATATCAAGATTCT 518
Db 18 ATTCATATCATATTTCAT 1
RESULT 896
AAT74905/c
ID AAT74905 standard; RNA; 19 BP.
XX
XX AAT74905;
AC
AT 27-AUG-1997 (first entry)
DT
XX
XX 5' end fragment of Alfalfa Mosaic Virus 4.
DE Alfalfa Mosaic virus 4; Influenza endonuclease; detection;
KW electrophoresis; substrate cleavage; ss..
XX
XX Alfalfa Mosaic virus 4.
XX
PH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= Triphosphorylated-G
FT modified_base 2 /*tag= b
FT /mod_base= 2'-OME-U
XX
XX WO9640994-A1.

19-DEC-1996.
03-JUN-1996; 96WO-US08330.
07-JUN-1995; 95US-0487760.
(MERI) MERCK & CO INC.
Cole JL, Kuo LC, Olsen DB;
WPI; 1997-052365/05.

Detection of enzyme pref. endonuclease or ribozyme, in a sample - by cleavage of an RNA substrate to generate a primer for a labelled polymerase extension reaction
Examples; Page 14; 34pp; English.

This sequence represents the 5' end of Alfalfa Mosaic virus 4 RNA. This sequence was used in the method of the invention for detecting the enzyme activity in a sample. The method comprises: (a) adding an oligonucleotide substrate to a sample to generate an oligonucleotide product; (b) hybridising the oligonucleotide prod. with a DNA template which comprises a first segment complementary to the oligonucleotide and a 5' extension of at least one nucleotide attached to the 5' end of the DNA segment, such that a DNA:RNA hybrid or a DNA:DNA duplex is formed; (c) adding a DNA polymerase and labelled mononucleotides such that the DNA polymerase incorporates the mononucleotides to the 3' end of the oligonucleotide; and (d) measuring the amt. of labelled hybrid prod. as a measure of the amt. of the enzyme activity in the sample. The method is used to assay for enzymes e.g. endonuclease, exonuclease or ribozymes, that act on substrates to generate single stranded oligonucleotide prods. by cleaving the substrate which then forms a primer for extension by a DNA polymerase on a template. It can be used to identify the position where the enzyme cleaves the substrate. The assay can also be used to screen for inhibitors of these enzymes.

Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;

Query Match 0.9%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 7.5e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1589 GAAATATATAAAAGTAAATA 1606
|||||
19 GAAATATATAAAATATAAA 2

RESULT 897
T49298/c
AAT49298 standard; RNA; 19 BP.
AAT49298;
27-AUG-1997 (first entry)
5' end fragment of Alfalfa Mosaic Virus 4.
Alfalfa Mosaic virus 4; influenza endonuclease; detection; electrophoresis; substrate cleavage; ss.
Alfalfa Mosaic virus 4.
WO9640993-A1.
19-DEC-1996.
03-JUN-1996; 96WO-US08330.
07-JUN-1995; 95US-0487759.
(MERI) MERCK & CO INC.

PI Cole JL, Kuo LC, Olsen DB;
XX WPI; 1997-052364/05.
DR
XX

PT Detection of influenza virus endonuclease in a sample - by cleavage of an RNA substrate to generate a primer for a labelled polymerase extension reaction
PT

XX Claim 6; Page 12; 28pp; English.
PS

XX This sequence represents the 5' end of Alfalfa Mosaic virus 4 RNA.
CC This sequence was used as a substrate for influenza endonuclease in the method of the invention. The method allows detection of influenza endonuclease activity in a sample and comprises: (a) adding an influenza endonuclease substrate to a sample to generate an RNA product; (b) hybridising the RNA prod. with a DNA template which comprises a first segment complementary to the RNA and a 5' extension of at least one nucleotide attached to the 5' end of the DNA segment, such that a DNA:RNA hybrid is formed; (c) adding a DNA polymerase and labelled mononucleotides such that the DNA polymerase incorporates the mononucleotides to the 3' end of the RNA in the RNA:DNA duplex; and (d) measuring the amount of labelled hybrid prod. as a measure of the amount of influenza endonuclease activity. The method is used to quantitate the amount of influenza endonuclease by cleaving the RNA substrate which then forms a primer for extension by a DNA polymerase on a template. The assay does not involve an electrophoresis step and thus may be run in a 96-well microtitre plate. The assay also monitors substrate cleavage at the correct position thereby discriminating against non-specific cleavage products.

XX Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;
SQ

Query Match 0.9%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 7.5e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1589 GAAATATATAAAAGTAAATA 1606
|||||
DB 19 GAAATATATAAAATATAAA 2

RESULT 898
AAT47269/c
ID AAT47269 standard; RNA; 19 BP.
XX
AC AAT47269;

XX 28-AUG-1997 (first entry)
XX Capped RNA influenza endonuclease substrate #3.
XX Capped RNA molecule; mRNA maturation; translation initiation; influenza; endonuclease aptamer; RNase; therapy; inhibitor; ss.
KW
XX Synthetic.

Key	Location/Qualifiers
modified_base 1	/tag= a
modified_base 2	/mod_base= triphosphorylated
modified_base 13	/tag= b
modified_base 13	/mod_base= 2'-O-methyluridine
modified_base 13	/tag= c
modified_base 13	/mod_base= 2'-deoxyadenosine

XX WO9640159-A1.
PN
XX 19-DEC-1996.
PD
XX 03-JUN-1996; 96WO-US08394.
PP
XX

R 07-JUN-1995; 95US-0480068.
X (MERI) MERCK & CO INC.
X Benseler F, Cole JL, Kuo LC, Olsen DB;
X WPI; 1997-051868/05.
X Production of capped RNA or analogues - useful as substrates for
X influenza virus associated virally encoded endonuclease
X Claim 18; Page 13; 39pp; English.
X AAT47264-T47280 represent capped RNA molecules produced by the method of
X the invention. The method of the invention is for producing capped RNA
X or RNA analogues. The method comprises reacting a RNA or analogue
X oligonucleotide with a phosphate addition agent to form a RNA or
X analogue mono-, di- or triphosphate, which is then capped. The presence
X of the cap is important for mRNA maturation, initiation of translation,
X and protects the mRNA against various RNases present in the cell. The
X capped RNA or analogue is an influenza endonuclease aptamer, useful for
X treating or preventing an influenza infection in an animal. The synthetic
X capped RNA are substrates for virally encoded endonuclease associated
X with influenza virus. The short non-extendible (due to their length or
X because of the modification of the 3' end of the oligo) RNA molecules are
X potent inhibitors of the cleavage of capped RNA by influenza
X endonuclease. They may be used to investigate viral and cellular
X mechanisms of transcription/translation, or mRNA maturation.
X Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;
Query Match 0.9%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 7.5e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Y 1589 GAAATATATAAGTAATAA 1606
b 19 GAAATATATAAGTAATAA 2

RESULT 899
LAT47270/C
ID AAT47270 standard; RNA; 19 BP.
X AAT47270;
X 28-AUG-1997 (first entry)
X Capped RNA influenza endonuclease substrate #4.
X Capped RNA molecule; mRNA maturation; translation initiation; influenza;
X endonuclease aptamer; RNase; therapy; inhibitor; ss.
X Synthetic.
X Key Location/Qualifiers
X modified_base 1 /*tag= a
X modified_base 2 /mod_base= triphosphorylated
X modified_base /*tag= b
X modified_base 13 /mod_base= 2'-O-methyluridine
X modified_base 13 /*tag= c
X modified_base 13 /mod_base= 2'-deoxy-2'-fluoro-adenosine
X WO9640159-A1.
X 19-DEC-1996.
X 03-JUN-1996; 96WO-US08394.
X 07-JUN-1995; 95US-0480068.

XX (MERI) MERCK & CO INC.
XX Benseler F, Cole JL, Kuo LC, Olsen DB;
XX WPI; 1997-051868/05.
XX Production of capped RNA or analogues - useful as substrates for
XX influenza virus associated virally encoded endonuclease
XX Claim 18; Page 13; 39pp; English.
XX AAT47264-T47280 represent capped RNA molecules produced by the method of
XX the invention. The method of the invention is for producing capped RNA
XX or RNA analogues. The method comprises reacting a RNA or analogue
XX oligonucleotide with a phosphate addition agent to form a RNA or
XX analogue mono-, di- or triphosphate, which is then capped. The presence
XX of the cap is important for mRNA maturation, initiation of translation,
XX and protects the mRNA against various RNases present in the cell. The
XX capped RNA or analogue is an influenza endonuclease aptamer, useful for
XX treating or preventing an influenza infection in an animal. The synthetic
XX capped RNA are substrates for virally encoded endonuclease associated
XX with influenza virus. The short non-extendible (due to their length or
XX because of the modification of the 3' end of the oligo) RNA molecules are
XX potent inhibitors of the cleavage of capped RNA by influenza
XX endonuclease. They may be used to investigate viral and cellular
XX mechanisms of transcription/translation, or mRNA maturation.
XX Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;
Query Match 0.9%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 7.5e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 1589 GAAATATATAAGTAATAA 1606
Db 19 GAAATATATAAGTAATAA 2

RESULT 900
AAT47271/C
ID AAT47271 standard; RNA; 19 BP.
XX AAT47271;
XX 28-AUG-1997 (first entry)
XX Capped RNA influenza endonuclease substrate #5.
XX Capped RNA molecule; mRNA maturation; translation initiation; influenza;
XX endonuclease aptamer; RNase; therapy; inhibitor; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX modified_base 2 /mod_base= triphosphorylated
XX modified_base /*tag= b
XX modified_base 6 /mod_base= 2'-O-methyluridine
XX modified_base /*tag= c
XX modified_base 12 /mod_base= 2'-deoxy-2'-fluoro-uridine
XX modified_base 12 /*tag= d
XX modified_base 12 /mod_base= 2'-deoxy-2'-fluoro-uridine
XX WO9640159-A1.
XX 19-DEC-1996.
XX 03-JUN-1996; 96WO-US08394.

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3 07-JUN-1995; 95US-0480068.
4 (MERI ) MERCK & CO INC.
5 Benseler F, Cole JL, Kuo LC, Olsen DB;
6 WPI; 1997-051868/05.
7 Production of capped RNA or analogues - useful as substrates for
8 influenza virus associated virally encoded endonuclease
9 Claim 18; Page 14; 39pp; English.
10 AAT47264-747280 represent capped RNA molecules produced by the method of
11 the invention. The method of the invention is for producing capped RNA
12 or RNA analogues. The method comprises reacting a RNA or analogue
13 oligonucleotide with a phosphate addition agent to form a RNA or
14 analogue mono-, di- or triphosphate, which is then capped. The presence
15 of the cap is important for mRNA maturation, initiation of translation,
16 and protects the mRNA against various RNases present in the cell. The
17 capped RNA or analogue is an influenza endonuclease aptamer, useful for
18 treating or preventing an influenza infection in an animal. The synthetic
19 capped RNA are substrates for virally encoded endonuclease associated
20 with influenza virus. The short non-extendible (due to their length or
21 because of the modification of the 3' end of the oligo) RNA molecules are
22 potent inhibitors of the cleavage of capped RNA by influenza
23 endonuclease. They may be used to investigate viral and cellular
24 mechanisms of transcription/translation, or mRNA maturation.
25 Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;
26
27 Query Match 0.9%; Score 11.6; DB 1; Length 19;
28 Best Local Similarity 77.8%; Pred. No. 7.5e+02;
29 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
30
31 1589 GAAATATATAAAGTAAATA 1606
32 ||||| ||||| |||||
33 19 GAAATATATAAAGTAAATA 2
34
35 RESULT 901
36 AAT47272/c
37 ID AAT47272 standard; RNA; 19 BP.
38 XX
39 AC AAT47272;
40 XX
41 DT 28-AUG-1997 (first entry)
42 XX
43 DE Capped RNA influenza endonuclease substrate #6.
44 XX
45 KW Capped RNA molecule; mRNA maturation; translation initiation; influenza;
46 endonuclease aptamer; RNase; therapy; inhibitor; ss.
47 Synthetic.
48
49 Key Location/Qualifiers
50 modified_base 1 /tag= a
51 /mod_base= triphosphorylated
52 modified_base 2 /tag= b
53 /mod_base= 2'-deoxy-2'-fluoro-uridine
54 modified_base 12 /tag= d
55 /mod_base= 2'-deoxy-2'-fluoro-uridine
56 modified_base 13 /tag= e
57 /mod_base= 2'-deoxy-2'-fluoro-adenosine

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PN WO9640159-A1.
XX
PD 19-DEC-1996.
XX
PF 03-JUN-1996; 96WO-US08394.
XX
PR 07-JUN-1995; 95US-0480068.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Benseler F, Cole JL, Kuo LC, Olsen DB;
XX WPI; 1997-051868/05.
XX
PT Production of capped RNA or analogues - useful as substrates for
PT influenza virus associated virally encoded endonuclease
XX
PS Claim 18; Page 14; 39pp; English.
XX
CC AAT47264-747280 represent capped RNA molecules produced by the method of
CC the invention. The method of the invention is for producing capped RNA
CC or RNA analogues. The method comprises reacting a RNA or analogue
CC oligonucleotide with a phosphate addition agent to form a RNA or
CC analogue mono-, di- or triphosphate, which is then capped. The presence
CC of the cap is important for mRNA maturation, initiation of translation,
CC and protects the mRNA against various RNases present in the cell. The
CC capped RNA or analogue is an influenza endonuclease aptamer, useful for
CC treating or preventing an influenza infection in an animal. The synthetic
CC capped RNA are substrates for virally encoded endonuclease associated
CC with influenza virus. The short non-extendible (due to their length or
CC because of the modification of the 3' end of the oligo) RNA molecules are
CC potent inhibitors of the cleavage of capped RNA by influenza
CC endonuclease. They may be used to investigate viral and cellular
CC mechanisms of transcription/translation, or mRNA maturation.
XX
SQ Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;
XX
XX
XX Query Match 0.9%; Score 11.6; DB 1; Length 19;
XX Best Local Similarity 77.8%; Pred. No. 7.5e+02;
XX Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1589 GAAATATATAAAGTAAATA 1606
XX ||||| ||||| |||||
XX Db 19 GAAATATATAAAGTAAATA 2
XX
XX RESULT 902
XX AAT47273/c
XX ID AAT47273 standard; RNA; 19 BP.
XX
XX AC AAT47273;
XX
XX DT 28-AUG-1997 (first entry)
XX
XX DE Capped RNA influenza endonuclease substrate #7.
XX
XX KW Capped RNA molecule; mRNA maturation; translation initiation; influenza;
XX endonuclease aptamer; RNase; therapy; inhibitor; ss.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1 /tag= a
XX /mod_base= triphosphorylated
XX modified_base 2 /tag= b
XX /mod_base= 2'-O-methyluridine
XX misc_feature 19
XX /tag= c
XX /note= "biotin labelled for attachment to solid support"
XX
XX WO9640159-A1.

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X 19-DEC-1996.
X 03-JUN-1996; 96WO-US08394.
X 07-JUN-1995; 95US-0480068.
X (MERI ) MERCK & CO INC.
X Benseler F, Cole JL, Kuo LC, Olsen DB;
X WPI; 1997-051868/05.
X Production of capped RNA or analogues - useful as substrates for
X influenza virus associated virally encoded endonuclease
X Claim 18; Page 14; 39pp; English.
X AAT47264-T47280 represent capped RNA molecules produced by the method of
X the invention. The method of the invention is for producing capped RNA
X or RNA analogues. The method comprises reacting a RNA or analogue
X oligonucleotide with a phosphate addition agent to form a RNA or
X analogue mono-, di- or triphosphate, which is then capped. The presence
X of the cap is important for mRNA maturation, initiation of translation,
X and protects the mRNA against various RNases present in the cell. The
X capped RNA or analogue is an influenza endonuclease aptamer, useful for
X treating or preventing an influenza infection in an animal. The synthetic
X capped RNA are substrates for virally encoded endonuclease associated
X with influenza virus. The short non-extendible (due to their length or
X because of the modification of the 3' end of the oligo) RNA molecules are
X potent inhibitors of the cleavage of capped RNA by influenza
X endonuclease. They may be used to investigate viral and cellular
X mechanisms of transcription/translation, or mRNA maturation.
X Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;
X
X Query Match 0.9%; Score 11.6; DB 1; Length 19;
X Best Local Similarity 77.8%; Pred. No. 7.5e+02;
X Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
X
X 1599 GAAATATATAAGTAAATA 1606
X ||||| ||||| ||||| |||||
X 19 GAAATATATAAGTAAATA 2
X
X RESULT 903
X AAT47267/C
X ID AAT47267 standard; RNA; 19 BP.
X AC AAT47267;
X DE 28-AUG-1997 (first entry)
X KW Capped RNA influenza endonuclease substrate #1.
X OS Capped RNA molecule; mRNA maturation; translation initiation; influenza;
X endonuclease aptamer; RNase; therapy; inhibitor; ss.
X Synthetic.
X Key Location/Qualifiers
X modified_base 1 /*tag= a
X /mod_base= triphosphorylated
X modified_base 2 /*tag= b
X /mod_base= 2'-O-methyluridine
X WO9640159-A1.
X 19-DEC-1996.
X 03-JUN-1996; 96WO-US08394.

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XX 07-JUN-1995; 95US-0480068.
XX (MERI ) MERCK & CO INC.
XX Benseler F, Cole JL, Kuo LC, Olsen DB;
XX WPI; 1997-051868/05.
XX Production of capped RNA or analogues - useful as substrates for
XX influenza virus associated virally encoded endonuclease
XX Claim 18; Page 13; 39pp; English.
XX AAT47264-T47280 represent capped RNA molecules produced by the method of
XX the invention. The method of the invention is for producing capped RNA
XX or RNA analogues. The method comprises reacting a RNA or analogue
XX oligonucleotide with a phosphate addition agent to form a RNA or
XX analogue mono-, di- or triphosphate, which is then capped. The presence
XX of the cap is important for mRNA maturation, initiation of translation,
XX and protects the mRNA against various RNases present in the cell. The
XX capped RNA or analogue is an influenza endonuclease aptamer, useful for
XX treating or preventing an influenza infection in an animal. The synthetic
XX capped RNA are substrates for virally encoded endonuclease associated
XX with influenza virus. The short non-extendible (due to their length or
XX because of the modification of the 3' end of the oligo) RNA molecules are
XX potent inhibitors of the cleavage of capped RNA by influenza
XX endonuclease. They may be used to investigate viral and cellular
XX mechanisms of transcription/translation, or mRNA maturation.
XX Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;
XQ
X Query Match 0.9%; Score 11.6; DB 1; Length 19;
X Best Local Similarity 77.8%; Pred. No. 7.5e+02;
X Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
X
X 1599 GAAATATATAAGTAAATA 1606
X ||||| ||||| ||||| |||||
X 19 GAAATATATAAGTAAATA 2
X
X RESULT 904
X AAT47264/C
X ID AAT47264 standard; RNA; 19 BP.
X AC AAT47264;
X DE 27-AUG-1997 (first entry)
X KW 5' fragment of alfalfa mosaic virus.
X OS Capped RNA molecule; mRNA maturation; translation initiation; influenza;
X endonuclease aptamer; RNase; therapy; inhibitor; ss.
X Synthetic.
X Key Location/Qualifiers
X modified_base 1 /*tag= a
X /mod_base= triphosphorylated
X modified_base 2 /*tag= b
X /mod_base= 2'-O-methyluridine
X WO9640159-A1.
X 19-DEC-1996.
X 03-JUN-1996; 96WO-US08394.
X 07-JUN-1995; 95US-0480068.
X (MERI ) MERCK & CO INC.

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Production of capped RNA or analogues - useful as substrates for influenza virus associated virally encoded endonuclease

S Claim 18; Page 15; 39pp; English.

X AAT47264-T47280 represent capped RNA molecules produced by the method of

C the invention. The method of the invention is for producing capped RNA

C or RNA analogues. The method comprises reacting a RNA or analogue

C oligonucleotide with a phosphate addition agent to form a RNA or

C analogue mono-, di- or triphosphate, which is then capped. The presence

C of the cap is important for mRNA maturation, initiation of translation,

C and protects the mRNA against various RNases present in the cell. The

C capped RNA or analogue is an influenza endonuclease aptamer, useful for

C treating or preventing an influenza infection in an animal. The synthetic

C capped RNA are substrates for virally encoded endonuclease associated

C with influenza virus. The short non-extendible (due to their length or

C because of the modification of the 3' end of the oligo) RNA molecules are

C potent inhibitors of the cleavage of capped RNA by influenza

C endonuclease. They may be used to investigate viral and cellular

C mechanisms of transcription/translation, or mRNA maturation.

X X

X Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;

Query Match 0.9%; Score 11.6; DB 1; Length 19;

Best Local Similarity 77.8%; Pred. No. 7.5e+02;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Y 1589 GAAATATATAAGTAAATA 1606

b ||||| ||||| ||||| |||||

19 GAAATATATAAGTAAATA 2

RESULT 907

AT47278/c

D AAT47278 standard; RNA; 19 BP.

X AAT47278;

X 28-AUG-1997 (first entry)

X Capped RNA influenza endonuclease substrate #10.

X Capped RNA molecule; mRNA maturation; translation initiation; influenza;

X endonuclease aptamer; RNase; therapy; inhibitor; ss.

X Synthetic.

X Key Location/Qualifiers

X modified_base 1 /*tag= a

X modified_base 2 /*mod_base= triphosphorylated

X modified_base 13 /*tag= b

X modified_base 14 /*mod_base= 2'-O-methyluridine

X /*tag= c

X /*mod_base= phosphorothioated

X WO9640159-A1.

X 19-DEC-1996.

X 03-JUN-1996; 96WO-US08394.

X 07-JUN-1995; 95US-0480068.

X (MERI) MERCK & CO INC.

X Benseler F, Cole JL, Kuo LC, Olsen DB;

X WPI; 1997-051868/05.

X Production of capped RNA or analogues - useful as substrates for

X influenza virus associated virally encoded endonuclease

X Claim 18; Page 15; 39pp; English.

XX AAT47264-T47280 represent capped RNA molecules produced by the method of

CC the invention. The method of the invention is for producing capped RNA

CC or RNA analogues. The method comprises reacting a RNA or analogue

CC oligonucleotide with a phosphate addition agent to form a RNA or

CC analogue mono-, di- or triphosphate, which is then capped. The presence

CC of the cap is important for mRNA maturation, initiation of translation,

CC and protects the mRNA against various RNases present in the cell. The

CC capped RNA or analogue is an influenza endonuclease aptamer, useful for

CC treating or preventing an influenza infection in an animal. The synthetic

CC capped RNA are substrates for virally encoded endonuclease associated

CC with influenza virus. The short non-extendible (due to their length or

CC because of the modification of the 3' end of the oligo) RNA molecules are

CC potent inhibitors of the cleavage of capped RNA by influenza

CC endonuclease. They may be used to investigate viral and cellular

CC mechanisms of transcription/translation, or mRNA maturation.

XX X

X Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;

Query Match 0.9%; Score 11.6; DB 1; Length 19;

Best Local Similarity 77.8%; Pred. No. 7.5e+02;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1589 GAAATATATAAGTAAATA 1606

Db ||||| ||||| ||||| |||||

19 GAAATATATAAGTAAATA 2

RESULT 908

AAT47279/c

ID AAT47279 standard; RNA; 19 BP.

XX AAT47279;

XX 28-AUG-1997 (first entry)

XX Capped RNA influenza endonuclease substrate #11.

XX Capped RNA molecule; mRNA maturation; translation initiation; influenza;

XX endonuclease aptamer; RNase; therapy; inhibitor; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX modified_base 1 /*tag= a

XX modified_base 2 /*mod_base= triphosphorylated

XX modified_base 12 /*tag= b

XX modified_base 13 /*mod_base= 2'-O-methyluridine

XX /*tag= c

XX /*mod_base= phosphorothioated

XX /*tag= d

XX /*mod_base= phosphorothioated

XX modified_base 14 /*tag= e

XX /*mod_base= phosphorothioated

XX WO9640159-A1.

XX 19-DEC-1996.

XX 03-JUN-1996; 96WO-US08394.

XX 07-JUN-1995; 95US-0480068.

XX (MERI) MERCK & CO INC.

XX Benseler F, Cole JL, Kuo LC, Olsen DB;

XX WPI; 1997-051868/05.

Production of capped RNA or analogues - useful as substrates for influenza virus associated virally encoded endonuclease

Claim 18; Page 15; 39pp; English.

AAT47264-747280 represent capped RNA molecules produced by the method of the invention. The method of the invention is for producing capped RNA or RNA analogues. The method comprises reacting a RNA or analogue oligonucleotide with a phosphate addition agent to form a RNA or analogue mono-, di- or triphosphate, which is then capped. The presence of the cap is important for mRNA maturation, initiation of translation, and protects the mRNA against various RNases present in the cell. The capped RNA or analogue is an influenza endonuclease aptamer, useful for treating or preventing an influenza infection in an animal. The synthetic capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extensible (due to their length or because of the modification of the 3' end of the oligo) RNA molecules are potent inhibitors of the cleavage of capped RNA by influenza endonuclease. They may be used to investigate viral and cellular mechanisms of transcription/translation, or mRNA maturation.

Sequence 19 BP; 3 A; 1 C; 1 G; 14 U; 0 other;

Query Match 0.9%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 7.5e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1589 GAAATATATAAGTAAATA 1606
19 GAAATATATAAGTAAATA 2

RESULT 909
AC92878
AAC92878 standard; DNA; 20 BP.

AAC92878;
27-MAR-2001 (first entry)

Human PI3 kinase p55 gamma antisense oligonucleotide, SEQ ID NO:61.
Human phosphatidylinositol 3-kinase p55 gamma regulatory subunit;
PI3 kinase p55 gamma, hp55-gamma, PIK3R3; p55PIK; kinase;
signal transduction; downstream effector; receptor tyrosine kinase;
insulin receptor; IR; insulin-like growth factor receptor; IGF1R;
cell growth; differentiation; apoptosis; developmental regulation;
alternative splicing; tumour formation; cancer; inflammation;
infection; expression inhibition; phosphorothioate;
antisense oligonucleotide; ss.

Homo sapiens.

US6165790-A.

26-DEC-2000.

03-NOV-1999; 99US-0433694.

03-NOV-1999; 99US-0433694.

(ISIS-) ISIS PHARM INC.

Borchers AH, Cowser LM, Ward DT;
WPI; 2001-101697/11.

Novel antisense compound targeted to human PI3 kinase p55 gamma specifically hybridizes with and inhibits the expression of human PI3 kinase p55 gamma, useful for modulating the expression of PI3 kinase p55 gamma in cells -

Example 15; Column 41-42; 39pp; English.

Sequences AAC92877-C92906 represent phosphorothioate antisense oligonucleotides targeted to the phosphatidylinositol 3-kinase p55 gamma regulatory subunit (PI3 kinase p55 gamma) gene, which inhibit its expression. The antisense oligonucleotides were designed to target different regions of human PI3 kinase p55 mRNA species, and were analysed for their effect on PI3 kinase p55 mRNA levels by quantitative real-time PCR. PI3 kinase p55 gamma (also known as hp55-gamma, p55-gamma, PIK3R3 and p55PIK) is one of several PI3 kinase regulatory subunits that may associate with the PI3 kinase catalytic subunit to form a heterodimeric PI3 kinase holoenzyme. PI3 kinases act as downstream effectors of receptor tyrosine kinases such as growth factor and hormone receptors and oncogene products, and are found in association with the cytoplasmic domains of such receptors. PI3 kinase p55 gamma is able to interact with both the insulin receptor (IR) and the insulin-like growth factor receptor (IGF1R), which play important roles in growth, differentiation and apoptosis. PI3 kinase p55 gamma is thought to be developmentally regulated, as four distinct mRNA species are found in adult tissues, while only the larger mRNA is expressed in foetal tissues. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with PI3 kinase p55 expression, such as tumour formation, inflammation and certain infections, and allow expression level modulation of the alternatively spliced forms of PI3 kinase p55.

Sequence 20 BP; 7 A; 1 C; 1 G; 11 T; 0 other;

Query Match 0.9%; Score 11.6; DB 1; Length 20;
Best Local Similarity 77.8%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1561 AATTTTCTTACTGTTC 1578
1 AATATTTTAAATGTTC 18

RESULT 910
ABK85435/C
ID ABK85435 standard; DNA; 20 BP.

AC ABK85435;
14-AUG-2002 (first entry)

Oligonucleotide #13 binding to specific site of HIV-1 RNA.
Human immunodeficiency virus type 1; HIV-1 detection method;
primer; probe; ss.
Human immunodeficiency virus type 1.

BP1203826-A2.

08-MAY-2002.

30-OCT-2001; 2001EP-0125378.

30-OCT-2000; 2000JP-0334937.

(TOYJ) TOSOH CORP.

Ishizuka T, Ishiguro T, Saitoh J;
WPI; 2002-473032/51.

An oligonucleotide useful for detection of an RNA derived from HIV-1 in clinical tests and diagnosis -

Claim 1; Page 16; 34pp; English.

The present invention relates to oligonucleotides binding to specific sites of human immunodeficiency virus type 1 (HIV-1) RNA. The

oligonucleotides are useful for detecting HIV-1 in clinical tests and diagnosis. The oligonucleotides provide simple, speedy and sensitive detection of HIV-1 RNA which can bind to an intramolecularly free region of the genomic RNA of HIV-1 at relatively low and constant temperatures. The detection method comprises synthesising a cDNA by the action of an RNA-dependent DNA polymerase by using a specific sequence in an RNA derived from HIV-1 antipated in a sample as a template, a first primer containing a sequence complementary to the specific sequence and a second primer containing a sequence homologous to the specific sequence (either of which additionally has a promoter sequence for the RNA polymerase at the 5' end). ABK85423-ABK85440 represent oligonucleotides binding to specific sites of HIV-1 RNA. They can be used either as first primers or probes.

Sequence 20 BP; 6 A; 2 C; 0 G; 12 T; 0 other;

Query Match 0.9%; Score 11.6; DB 1; Length 20;

Best Local Similarity 77.8%; Pred. No. 7.6e+02;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Y 1590 AAATATAAAAGTAAAT 1607

||||| ||||| ||

18 AAATAAATAGTAAAT 1

RESULT 911

BL51148

ABL51148 standard; DNA; 20 BP.

X ABL51148;

X ABL51148;

X ABL51148;

T 27-JUN-2002 (first entry)

Human TNF inducible protein A20 antisense oligonucleotide SEQ ID:26.

Human; tumour necrosis factor inducible protein A20; phosphorothioate; antisense modulation; antisense oligonucleotide; antiinflammatory; cytoskeletal; antiviral; gene therapy; TNF inducible protein A20; inflammatory disorder; viral infection; hyperproliferative disorder; cancer; inflammation; tumour formation; ss.

Homo sapiens.

Synthetic.

Key Location/Qualifiers

modified_base 1..20

/*tag= a

/mod_base= OTHER

/note= "2'-methoxyethyl (MOE) nucleotide wings and a

deoxy gap with a phosphorothioate backbone"

modified_base 1..5

/*tag= b

/mod_base= OTHER

/note= "2'-O-methoxyethyl nucleotides"

modified_base 15..20

/*tag= c

/mod_base= OTHER

/note= "2'-O-methoxyethyl nucleotides"

W0200220545-A1.

14-MAR-2002.

07-SEP-2001; 2001WO-US28116.

08-SEP-2000; 2000US-0658687.

(ISIS-) ISIS PHARM INC.

Bennett CF, Wyatt JR;

WPI; 2002-362238/39.

PT New antisense compound useful for preventing or delaying infection, inflammation or tumor formation, hybridizes and inhibits a nucleic acid molecule encoding tumor necrosis factor inducible protein, A20 -

Claim 3; Page 91; 121pp; English.

The present invention describes a compound (I) of 8 - 50 nucleotides targeted to a nucleic acid molecule (II) encoding tumour necrosis factor (TNF) inducible protein, A20, and which specifically hybridises with and inhibits expression of A20, or a compound (Ia) of 8 - 50 nucleotides which specifically hybridises with an 8-nucleotide portion of an active site on (II). (I) have antiinflammatory, cytostatic and antiviral activities. (I) can be used as inhibitors of TNF inducible protein, A20. (I) is useful for inhibiting the expression of A20 in cells or tissues, and for treating an animal having a disease condition associated with A20, e.g. a inflammatory disorder, viral infection and hyperproliferative disorder e.g. cancer. (I) is also useful prophylactically, e.g. to prevent or delay infection, inflammation or tumour formation. (I) is also useful as therapeutic, diagnostic and research reagent, for distinguishing functions of various members of a biological pathway, and in antisense gene therapy. The present sequence represents an antisense oligonucleotide for human TNF inducible protein A20, from the present invention.

Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 other;

Query Match 0.9%; Score 11.6; DB 1; Length 20;

Best Local Similarity 77.8%; Pred. No. 7.6e+02;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1289 TTTATCTGAAATTTTAAAT 1306

||||| ||||| |||||

1 TTTGCTGAAATGCAAT 18

RESULT 912

AAQ75568

ID AAQ75568 standard; DNA; 20 BP.

XX AAQ75568;

XX AAQ75568;

DT 04-AUG-1995 (first entry)

Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; CDNA; aggregate; restriction enzyme; ss.

Synthetic.

JP06303997-A.

01-NOV-1994.

16-APR-1993; 93JP-0112515.

16-APR-1993; 93JP-0112515.

(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

WPI; 1995-018287/03.

Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes

Disclosure; Page 5; 11pp; Japanese.

A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction

enzyme and, (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.

Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
 Query Match 0.9%; Score 11.6; DB 1; Length 20;
 Best Local Similarity 77.8%; Pred. No. 7.6e+02;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 1563 TTTTCTTACGTTCTG 1580
 |||||
 1 TTTTCTTCTTTTCTG 18

SULT 913
 T47265/C
 AAT47265 standard; RNA; 20 BP.
 AAT47265;
 27-AUG-1997 (first entry)
 5' fragment #2 of alfalfa mosaic virus.
 Capped RNA molecule; mRNA maturation; translation initiation; influenza; endonuclease aptamer; RNase; therapy; inhibitor; ss.
 Synthetic.

Key Location/Qualifiers
 modified_base 1 /*tag= a
 /mod_base= 7-methylguanosine
 modified_base 2 /*tag= b
 /mod_base= triphosphorylated
 modified_base 3 /*tag= c
 /mod_base= 2'-O-methyluridine

WO9640159-A1.
 19-DEC-1996.
 03-JUN-1996; 96WO-US08394.
 07-JUN-1995; 95US-0480068.
 (MERI) MERCK & CO INC.
 Benseler F, Cole JL, Kuo LC, Olsen DB;
 WPI; 1997-051868/05.
 Production of capped RNA or analogues - useful as substrates for influenza virus associated virally encoded endonuclease
 Claim 18; Page 12; 39pp; English.

AAT47264-T47280 represent capped RNA molecules produced by the method of the invention. The method of the invention is for producing capped RNA or RNA analogues. The method comprises reacting a RNA or analogue oligonucleotide with a phosphate addition agent to form a RNA or analogue mono-, di- or triphosphate, which is then capped. The presence of the cap is important for mRNA maturation, initiation of translation, and protects the mRNA against various RNases present in the cell. The capped RNA or analogue is an influenza endonuclease aptamer, useful for treating or preventing an influenza infection in an animal. The synthetic capped RNA are substrates for virally encoded endonuclease associated with influenza virus. The short non-extendible (due to their length or because of the modification of the 3' end of the oligo) RNA molecules are potent inhibitors of the cleavage of capped RNA by influenza

CC endonuclease. They may be used to investigate viral and cellular mechanisms of transcription/translation, or mRNA maturation.
 XX
 SQ Sequence 20 BP; 3 A; 1 C; 2 G; 14 U; 0 other;
 Query Match 0.9%; Score 11.6; DB 1; Length 20;
 Best Local Similarity 77.8%; Pred. No. 7.6e+02;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1589 GAAATATATAAGTAAATA 1606
 |||||
 DB 20 GAAATTTAAAAATAAAA 3
 RESULT 914
 AAV67374
 ID AAV67374 standard; DNA; 21 BP.
 XX
 AC AAV67374;
 XX
 DT 21-DEC-1998 (first entry)
 XX
 DE Nucleotide fragment containing polymorphic site, WI-5865 (1).
 XX
 KW ss; polymorphic site; nucleic acid analysis; diagnosis; monitoring; cancer; inflammation; heart disease; CNS disease.
 XX
 OS Homo sapiens.
 XX
 PN WO9838846-A2.
 XX
 PD 11-SEP-1998.
 XX
 PF 06-MAR-1998; 98WO-US04571.
 XX
 PR 28-MAR-1997; 97US-0042125.
 XX
 PR 07-MAR-1997; 97US-0813159.
 XX
 PA (APFY-) APFYMATRIX INC.
 XX
 PI Berno A, Chee M, Fan J, Lipschutz RJ;
 XX
 DR WPI; 1998-495419/42.
 XX
 PT New nucleic acid segments containing polymorphic sites, or complements and methods of detecting a nucleic acid - for general use including diagnosis and monitoring of diseases
 XX
 PS Claim 1; Page 9; 42pp; English.
 XX
 CC New nucleic acid segment comprising one of the 10 - 100 bp sequences given in the specification (sequences of a polymorphic site), or the complement of the segment and a method of analysing a nucleic acid comprising determining the base occupying the polymorphic site of the polymorphic fragment sequences are disclosed in the specification. The information obtained from nucleic acid analysis by the method described is useful in diagnosis or monitoring of diseases like cancer, inflammation, heart disease, CNS diseases, and susceptibility to infection by microorganisms. In addition, the nucleic acid segments are useful in manufacturing medication in the treatment of prophylaxis of diseases, and also the use of the DNA segments as pharmaceutical.
 XX
 SQ Sequence 21 BP; 13 A; 2 C; 0 G; 5 T; 1 other;

Query Match 0.9%; Score 11.6; DB 1; Length 21;
 Best Local Similarity 70.0%; Pred. No. 7.8e+02;
 Matches 14; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 613 TCTACAAAAAACCAATA 632
 |||||
 DB 1 TATCAAAATTAACCAATA 20

Beaudry A, Beigelman L, Beillon L, Burgin A, Jarvis T;
Karpeisky A, Kirsch K, Matulic-Adamic J, McGSwiggen JA;
Parry T, Reynolds M, Sweedler D, Thompson J, Workman CT;
WPI: 1999-009494/01.

Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, reutenosid, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons

Claim 177; Page 154; 259pp; English.

A method has been developed for the identification of a nucleic acid capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endonuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, perioris, non-hepatic ascites and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine c-rat RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, perioris or rheumatoid arthritis, or generally any condition associated with the level of c-rat. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. AA959322 to AA93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene.

Sequence 17 BP; 12 A; 0 C; 0 G; 5 U; 0 other;

Query Match 0.9%; Score 11.4; DB 1; Length 17;
Best Local Similarity 61.5%; Pred. No. 7.6e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

02 ATACATATAATTA 1014
|:|:|:|:|:|:|:
2 AUAAAAUAAAUUA 14

SULT 918
X70035/C
AAX70035 standard; RNA; 17 BP.
AAX70035;

28-JUL-1999 (first entry)

Human flt1 VEGF receptor hammerhead ribozyme substrate #1330.

Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor; foetal liver kinase 1; ss.

Homo sapiens.
WC09715662-A2.

01-MAY-1997.

25-OCT-1996; 96WO-US17480.

11-JAN-1996; 96US-0584040.

11-044-1330; 36US-0384040;
26-OCT-1995; 95US-0005974;

PA (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.

AA Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
PI
XX
DR WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 XT mRNA stability - useful for treating e.g. tumour angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 PT
 XX Claim 4; Page 86; 218pp; English.
 PS

The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX5752 represent specific examples of nucleic acid molecules from the present invention.

Sequence 17 BP; 9 A; 2 C; 0 G; 6 U; 0 other; 0 XA
SQ

Query Match 0.9%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 7.6e+02;
Matches 12: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	522	TAAATT	GAATT	534
Db	16	TAAATT <td>TGAGTT <td>4</td> </td>	TGAGTT <td>4</td>	4

RESULT 919
AAA21376/C

AAA21376/C
ID AAA21376 standard; RNA; 17 BP.

XX
AC

19-JUN-2000 {first entry}

Integrin alpha 6 subunit substrate sequence SEQ ID NO:4602.

Human; aryl hydrocarbon nuclear transport; ARNT, TTE-2, angiogenesis;
integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
immunomodulatory; antiarthritic; antipsoriatic; AMD;
ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; AMD;
dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
age related macular degeneration; inflammation; neovascular glaucoma;
myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
tuberculous scleritis; pot-wine stain; Sturge Weber syndrome;
Kipfel-Trenauer-Weber syndrome; Ogler-Weber-Rendu syndrome; ss.

Homo sapiens.

AA
PN
WO9950403-A2.

07-OCT-1999.

24-MAR-1999; 99WO-US06507.

27-MAR-1998: 98US-0079678.

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts B, Jarvis T, Coeshott C, McSwiggen JA;

XX
OR WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an oncogenic factors --

X	Claim 55; Page 204; 305pp; English.
S	The present invention describes enzymatic cleavage of nucleic acid molecules with
S	RNA cleaving activity, which specifically cleave RNA encoded by an aryl
C	hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
C	gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAL16775 to
C	AAL1767 and AAL19561 to AAL17622 represent ribozyme sequences for ARNT,
C	and AAL1768 to AAL19560 and AAL17623 to AAL17684 represent their
C	corresponding target sequences; AAL17685 to AAL18385 and AAL19087 to
C	AAL19154 represent ribozyme sequences for Tie-2, and AAL18386 to AAL19086
C	and AAL19155 to AAL19222 represent their corresponding target sequences;
C	AAL19223 to AAL20361 and AAL21501 to AAL21595 represent ribozyme
C	sequences for integrin alpha 6 subunit, and AAL20362 to AAL21500 and
C	AAL21596 to AAL21688 represent their corresponding target sequences;
C	AAL21689 to AAL22475 and AAL23263 to AAL23342 represent ribozyme sequence
C	for integrin subunit beta 3, and AAL22476 to AAL23262, AAL23343 to
C	AAL23422 represent their corresponding target sequences. The ribozymes of
C	the invention are used for modulating the synthesis, expression and/or
C	stability of an mRNA encoding angiogenic factor, especially ARNT,
C	integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
C	especially used to treat cancer, diabetic retinopathy, age related
C	macular degeneration [ARM], inflammation, and arthritis, as well as
C	neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
C	angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
C	syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
C	and other syndromes and diseases related to the levels of ARNT, Tie-2,
C	C integrin subunit alpha-6, or integrin subunit beta-3.
X	Sequence 17 BP; 6 A; 1 C; 1 G; 9 U; 0 other;
Q	
	Query Match 0.9%; Score 11.4; DB 1; Length 17;
	Best Local Similarity 92.3%; Pred. No. 7.6e+02;
	Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Y	1617 AAATATAATTGTTG 1629
b	{ }
	13 AAATATAATTGTTG 1
RESULT 920	
AS09117	
D AD	AA0909117 standard; DNA; 20 BP.
S .C	AA0909117;
.JT	26-SEP-2001 {first entry}
.X	Human MEKK2 antisense oligonucleotide 113923.
.DE	Human; Mitogen-activated protein kinase kinase 2; MAP; MEKK2;
.W	MEK kinase 2; MAP/ERK kinase kinase 2; immunological disorder;
.W	inflammatory disorder; hyperproliferative disorder; cancer; antisense;
.W	phosphorothioate; ss.
.X	Homo sapiens.
.XS	
.H	Key location/Qualifiers
.T	modified_base 1..20
.T	/*tag= a
.T	/mod base= "OTHER"
.T	/note= "OTHER- phosphorothioate internucleotide linkages.
.T	Some bases especially bases 1-5 and bases 16-20
.T	are 2'-methoxyethyl (2'-MOE) bases, bases 6-15
.T	are 2'-deoxynucleotides and all cytidine bases
.T	are 5'-methylcytidines"
.CX	
.CN	WO200152863-A1.
.PN	
.PD	26-JUL-2001.
.PF	16-JAN-2001; 2001WO-US01361.
.X	

```

14 modified_base      /*tag= f
/*mod_base= OTHER
16 modified_base      /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
17 /*tag= g
/*mod_base= OTHER
18 modified_base      /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
19 /*tag= h
/*mod_base= OTHER
20 modified_base      /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
21 /*tag= i
/*mod_base= OTHER
22 modified_base      /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
W09209705-A1.
11-JUN-1992.
25-NOV-1991; 91WO-US08811.
23-NOV-1990; 90US-0617907.
18-JAN-1991; 91US-0643382.
08-APR-1991; 91US-0683420.
17-APR-1991; 91US-0686544.
17-APR-1991; 91US-0686546.
17-APR-1991; 91US-0686547.
27-SEP-1991; 91US-0766733.
(GILE-) GILEAD SCI INC.

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Frøehler B, Krawczyk S, Matteucci MD, Milligan J;

WPI; 1992-217083/26.

New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes, malignancy and inflammation

Claim 12; Page 71; 77pp; English.

The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human interleukin-2 receptor gene exon 8 target and flanks beginning at nucleotide 114 contg. a purine rich sequence concd. on one strand of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV; HER; HIV; hepatitis B, herpes, malignant tumours and inflammation. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions.

See also AAQ25452-25501 and AAQ30226-448.

(Updated on 25-MAR-2003 to correct FN field.)

Sequence 21 BP; 9 A; 0 C; 0 G; 12 T; 0 other;

Query Match 0.9%; Score 11.4; DB 1; Length 21;
Best Local Similarity 71.4%; Pred.No.8.3e+02;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

997 TCATCATACATTAATTTT 1017
|||||
21 TAATTAATAATAATTAATT 1

```

SULT 922
226565/C
AAZ26565 standard; DNA; 21 BP.
AAZ26565;

```

XX 30-NOV-1999 (first entry)
XX Human polymorphic region 754.
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX allele viability; loss of heterozygosity; precancerous condition; ASI;
XX allele specific inhibitor; somatic cell; diagnosis; prevention;
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX graft versus host disease; malignant cell removal; bone marrow; ss.
XX Homo sapiens.
XX W09841648-A2.
XX 24-SEP-1998.
XX 19-MAR-1998; 98WO-US05419.
XX 20-MAR-1997; 97US-0041057.
XX (VARI-) VARIAGENICS INC.
XX Housman D, Ledley FD, Stanton VP;
XX WPI; 1998-521232/44.

```

Identifying target genes for allele-specific drugs - used for

diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic

plaque, dysplastic lesions, endometriosis or graft versus host disease

Disclosure; Figure 7; 605pp; English.

This invention describes a novel method for identifying an inhibitor potentially useful for treatment of cancer, where the inhibitor is active on a gene vital for cell growth or viability, and where the gene is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is used for preventing the development of cancer in a patient having a precancerous condition, by administering to the patient a first allele specific inhibitor (ASI) targeted to an allele of a first essential gene present in cells of the precancerous condition, where the normal somatic cells of the patient are heterozygous for the first gene, the inhibitor is active on at least one but less than all allelic forms of the gene present in a population and targets only one allelic form present in the normal somatic cells, and the first gene. The products and methods can be used in the diagnosis, prevention and treatment of LOH disorders, e.g. cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic lesions, benign tumours, endometriosis, polycystic kidney disease, and graft versus host disease. The method can also be used to remove malignant cells from bone marrow transplants. AAZ25812-226825 represent human polymorphic sites described in the method of the invention.

SQ Sequence 21 BP; 8 A; 1 C; 0 G; 12 T; 0 other;

Query Match 0.9%; Score 11.4; DB 1; Length 21;
Best Local Similarity 71.4%; Pred.No.8.3e+02;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

Qy 1200 TTACATTAACAAACAAACAA 1220
|||||
Db 21 TTATGTTAAAAATATAATAA 1

```

RESULT 923
AAA74329
ID AAA74329 standard; DNA; 16 BP.
XX
AC AAA74329;
XX
DT 29-NOV-2000 (first entry)
XX

The sequences given in AAT40327-30 represent sequences that were used to optimise DNA cleavage activity of the enzymatic RNA molecule of the invention. The 3' portion of the substrate was transferred to the 3' terminal G of the ribozyme and amplification was performed. The product of the reaction was a molecule which contained the 3' portion of the substrate attached to the 3' end of the ribozyme. Selection occurred when a primer was hybridised across the ligation junction and used to initiate cDNA synthesis. The primer does not bind to unreacted starting materials and thus led to selective amplification of the catalytically active RNA's. The self-splicing group I intron of the invention is based on the large ribosomal RNA precursor from *Tetrahymena thermophila*. The biological function of this molecule is to catalyse its own excision from precursor rRNA to produce mature rRNA. The *Tetrahymena* wild type sequence was used in the design of the enzymatic RNA molecules of the invention. A number of mutations are listed in the specification which improve the enzymatic properties of this molecule, e.g. G444A, G191U, U190A and A314G. The modified enzymatic molecules may be used as medical or pharmaceutical agents for use in anti-viral agents, food products, personal care products or cleaning agents.

Sequence 16 BP; 3 A; 1 C; 0 G; 12 T; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1589 GAAATATATAAAAGTAAA 1604
||||| |||||
16 GAAATATAAATAATAAA 1

RESULT 926

AAV09052/c
AAV09052 standard; DNA; 16 BP.

AAV09052;

25-JUN-1998 (first entry)

Primer 1 for *tetrahymena* ribozyme L-21.

Tetrahymena ribozyme; group I intron; amide end hydrolysis; peptidase; processase; antiviral agent; gene regulator; immunogenic virus; vaccine; mutation detection; PCR primer; ss.

Synthetic.

Tetrahymena sp.

WO9802583-A1.

22-JAN-1998.

16-JUL-1997; 9WO-US12394.

17-JUL-1996; 96US-0682423.

(SCRI) SCRIPPS RES INST.

Joyce GF;

WPI; 1998-110627/10.

Catalytic RNA for site-specific cleavage of nucleic acid or hydrolysis of amide bonds - and ribozyme amidease intermediates, useful e.g. as peptidase(s), antiviral agents and gene regulators

Example 1; Page 92; 215pp; English.

This sequence is a primer for a wild type *tetrahymena* ribozyme L-21 form. The amplified sequence is an example of a catalytic RNA (I) of the invention, which catalyses site-specific cleavage of nucleic acid under physiological conditions includes a sequence derived from a group I intron. Similar catalytic RNAs (II) which catalyse hydrolysis of amide

ends are useful as peptidases and proteases, e.g. in wound debridement, clot dissolution, in detergents or as a meat tenderiser. (I) cleave single- and (partly) double-stranded nucleic acids in vitro or in vivo, and are potentially useful as antiviral agents and gene regulators; also, to generate defective but still immunogenic viruses (for vaccines); CC diagnostically to detect mutations in nucleic acid or to identify nucleic acid binding agents; to modulate/terminate reactions initiated by DNA CC primers; to generate truncated transcripts from DNA; to modulate CC therapeutic/diagnostic processes using antisense sequences; in DNA CC fingerprinting and for vector construction. (I) and (II) are produced by CC in vitro evolution processes that provide better catalytic performance; CC broader active temperature and pH ranges; new enzymatic activities or CC specificities; altered recognition sites or co-factor requirement.

Sequence 16 BP; 3 A; 1 C; 0 G; 12 T; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 16;

Best Local Similarity 81.2%; Pred. No. 7.9e+02; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1589 GAAATATATAAAAGTAAA 1604
||||| |||||
Db 16 GAAATATAAATAATAAA 1

RESULT 927

AAA22698/c

ID AAA22698 standard; RNA; 17 BP.

XX AAA22698;

DT 19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SEQ ID NO:5924.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; age related macular degeneration; cancer; diabetic retinopathy; arthritis; myopic degeneration; psoriasis; verruca vulgaris; neovascular glaucoma; tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

XX WO9950403-A2.

XX 07-OCT-1999.

XX 24-MAR-1999; 99WO-US06507.

XX 27-MAR-1998; 98US-0079678.

XX (RIBO-) RIBOZYME PHARM INC.

XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;

XX WPI; 1999-591315/50.

XX Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors -

XX Claim 54; Page 236; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transport (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to

CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequences
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 X
 Q Sequence 17 BP; 5 A; 0 C; 0 G; 12 U; 0 other;
 Query Match 0.9%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 8.1e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Y 1206 TAAACAAACAAACANT 1221
 b 17 TAAATAATAATAATAAT 2
 ENUIT 928
 AAA22699/C
 D AAA22699 standard; RNA; 17 BP.
 X
 C AAA22699;
 X
 T 19-JUN-2000 (first entry)
 X
 E Integrin subunit beta 3 substrate sequence SEQ ID NO:5925.
 W Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
 W integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 W hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 W ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 W dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 W age related macular degeneration; inflammation; neovascular glaucoma;
 W myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 W tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
 W Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 X
 S Homo sapiens.
 X
 N WO9950403-A2.
 D 07-OCT-1999.
 X
 F 24-MAR-1999; 99WO-US06507.
 X
 R 27-MAR-1998; 98US-0079678.
 X
 A (RIBO-) RIBOZYME PHARM INC.
 T Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 R WPI; 1999-591315/50.
 X
 T Novel ribozymes for modulating the synthesis, expression and/or
 T stability of an mRNA encoding an angiogenic factors -
 X
 S Claim 54; Page 237; 305pp; English.
 X
 C The present invention describes enzymatic nucleic acid molecules with
 C RNA cleaving activity, which specifically cleave RNA encoded by an aryl

CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequences
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 X
 SQ Sequence 17 BP; 4 A; 0 C; 0 G; 13 U; 0 other;
 Query Match 0.9%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 8.1e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1591 AATATAAAGTAAATA 1606
 b 17 AATATAAATAATAATA 2
 RESULT 929
 AAA22701/C
 ID AAA22701 standard; RNA; 17 BP.
 X
 X AAA22701;
 AC
 DT 19-JUN-2000 (first entry)
 X
 E Integrin subunit beta 3 substrate sequence SEQ ID NO:5927.
 W Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
 W integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 W hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 W ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 W dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 W age related macular degeneration; inflammation; neovascular glaucoma;
 W myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 W tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
 W Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 X
 S Homo sapiens.
 X
 N WO9950403-A2.
 D 07-OCT-1999.
 X
 F 24-MAR-1999; 99WO-US06507.
 X
 R 27-MAR-1998; 98US-0079678.
 X
 A (RIBO-) RIBOZYME PHARM INC.
 T Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 R WPI; 1999-591315/50.
 X
 T Novel ribozymes for modulating the synthesis, expression and/or
 T stability of an mRNA encoding an angiogenic factors -

Claim 54; Page 237; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086 and AAA19155 to AAA19222 represent their corresponding target sequences; AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and AAA21596 to AAA21688 represent their corresponding target sequences; AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequences for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to AAA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 5 A; 0 C; 0 G; 12 U; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1590 AATATATAAAGCTAAAT 1605
||||| |||||
16 AATATAATAATAAATA 1

RESULT 930

AAA22702/c
AAA22702 standard; RNA; 17 BP.

AAA22702;

19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SEQ ID NO:5928.

Human; aryl hydrocarbon nuclear transporter; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

WO9950403-A2.

07-OCT-1999.

24-MAR-1999; 99WO-US06507.

27-MAR-1998; 98US-0079678.

(RISO-) RIBOZYME PHARM INC.

Pavco PA, Roberts B, Jarvis T, Coeshott C, McSwiggen JA;

XX

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors -
Claim 54; Page 237; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086 and AAA19155 to AAA19222 represent their corresponding target sequences; AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and AAA21596 to AAA21688 represent their corresponding target sequences; AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequences for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to AAA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 4 A; 0 C; 0 G; 13 U; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1591 AATATAAAGCTAAATA 1606
||||| |||||
Db 17 AATAATAATAATAATA 2

RESULT 931

AAA22704/c

ID AAA22704 standard; RNA; 17 BP.

AC AAA22704;

19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SEQ ID NO:5930.

Human; aryl hydrocarbon nuclear transporter; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

WO9950403-A2.

07-OCT-1999.

24-MAR-1999; 99WO-US06507.

XX

27-MAR-1998; 98US-0079678.
(RIBO-) RIBOZYME PHARM INC.
Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
WPI; 1999-591315/50.
Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors -
Claim 54; Page 237; 305pp; English.
The present invention describes enzymatic cleavage of nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT, and AA17168 to AA17560 and AA17623 to AA17684 represent their corresponding target sequences; AA17685 to AA18385 and AA19087 to AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086 represent their corresponding target sequences; AA19155 to AA19222 represent their corresponding target sequences; AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and AA21596 to AA21688 represent their corresponding target sequences; AA21689 to AA22475 and AA22476 to AA22477 represent ribozyme sequences for integrin subunit beta 3, and AA22478 to AA22479 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiobroma of tuberosus sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.
Sequence 17 BP; 5 A; 0 C; 0 G; 12 U; 0 other;
Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Y 1590 AAATATAAAGTAAAT 1605
b 16 AAATAATAATAATAAT 1
|||||
RESULT 932
AA22705/c
D AAA22705 standard; RNA; 17 BP.
X AAA22705;
X
T 19-JUN-2000 (first entry)
X Integrin subunit beta 3 substrate sequence SEQ ID NO:5931.
X Human; aryl hydrocarbon nuclear transporter; ARNT; TIE-2; angiogenesis;
X integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
X hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
X opthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
X dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
X age related macular degeneration; inflammation; neovascular glaucoma;
X myopic degeneration; psoriasis; verruca vulgaris; angiobroma;
X tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
X Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
X Homo sapiens.
X WO9950403-A2.

XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US06507.
XX
XX 27-MAR-1998; 98US-0079678.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
XX
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors -
XX
XX Claim 54; Page 237; 305pp; English.
XX The present invention describes enzymatic cleavage of nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT, and AA17168 to AA17560 and AA17623 to AA17684 represent their corresponding target sequences; AA17685 to AA18385 and AA19087 to AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086 represent their corresponding target sequences; AA19155 to AA19222 represent their corresponding target sequences; AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and AA21596 to AA21688 represent their corresponding target sequences; AA21689 to AA22475 and AA22476 to AA22477 represent ribozyme sequences for integrin subunit beta 3, and AA22478 to AA22479 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiobroma of tuberosus sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.
XX Sequence 17 BP; 4 A; 0 C; 0 G; 13 U; 0 other;
XX
XX Query Match 0.9%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 8.1e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1591 AATATAAAGTAAATA 1606
Db 17 AATATAATAATAATA 2
|||||
RESULT 933
AAD49640/c
ID AAD49640 standard; mRNA; 17 BP.
XX
XX AAD49640;
XX
XX 24-MAR-2003 (first entry)
XX Human adenylate uridylylate-rich element (ARE) motif mRNA #2.
XX
XX Amyloidosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer;
XX 9-ganglioneuroma; hypothyroidism; hyperthyroidism; cystic fibrosis;
XX autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic;
XX neurodegenerative disorder; Parkinson's disease; gene therapy; viricide;
XX haemostatic; antibacterial; nontropic; neuroprotective; cytostatic;
XX fungicide; human; adenylate uridylylate-rich element; ARE; ss.
XX Homo sapiens.
XX OS

WO200283953-A1.

24-OCT-2002.

11-APR-2002; 2002WO-US11757.

11-APR-2001; 2001US-282965P.

(PTCT-) PTC THERAPEUTICS INC.

Rando R, Welch E;

WPI; 2003-075561/07.

Identifying a test compound that binds to a target RNA molecule for treating or preventing amyloidosis, hemophilia, cancer, gigantism, diabetes, by contacting a detectably labeled target RNA molecule with a library of test compounds.

Disclosure; Page 18; 152pp; English.

The invention relates to a method for identifying a test compound that binds to a target RNA molecule, which comprises contacting a detectably labelled target RNA molecule with a library of test compounds under conditions that permit direct binding of the labelled target RNA to a member of the library of test compounds so that a detectably labeled target RNA: test compound complex is formed. The method is useful for screening libraries of compounds for those that are selectively bind to a pre-selected target RNA. The compounds are useful for inhibiting the formation of a specific bound RNA: host cell factor complexes in vivo. They are also useful for treating or preventing diseases associated with overproduction or decreased protein function, such as amyloidosis, haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism, dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging, inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative disorders, Parkinson's disease or infections (bacterial, viral, fungal). The invention is also used in gene therapy. The present sequence is human adenylate uridylylate-rich element (ARE) motif mRNA. This sequence is used to illustrate the method of the invention.

Sequence 17 BP; 5 A; 0 C; 0 G; 12 U; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. NO. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1590 AAATATATAAACTAAAT 1605
||||| |||||
16 AAATATAATAATAAT 1

SULT 934

L50229/c
AAL50229 standard; mRNA; 17 BP.

AAL50229;

13-FEB-2003 (first entry)

Human ARE-mRNA sequence #2.

ARE-mRNA; protein secretion inhibition; ARE-mRNA regulation; inflammation; arthritis; autoimmune disease; septic shock; blood clot; stroke; TNFalpha; tumour necrosis factor alpha; antiinflammatory; antiarthritis; antibacterial; immunosuppressive; cerebroprotective; antipyretic; immunomodulator; adenylate-uridylylate rich element; ss.

Homo sapiens.

WO200283842-A2.

24-OCT-2002.

XX 08-APR-2002; 2002WO-US10898.

XX 10-APR-2001; 2001US-282974P.

XX (MESS-) MESSAGE PHARM INC.

XX Giordano T, Sturges MA;

XX WPI; 2003-046924/04.

XX Modulating Adenylate-Uridylate Rich element-mRNA regulation involves administering new amide compound that inhibits secretion of protein encoded by ARE-mRNA, useful for treating inflammation, arthritis and autoimmune diseases.

XX Disclosure; Fig 5; 147pp; English.

XX The present invention relates to a method of modulating the regulation of an adenylate-uridylylate rich element (ARE)-mRNA, which involves administering new compounds that inhibits secretion of a protein encoded by an ARE-mRNA. This can be used in the treatment of inflammation, fever, arthritis, autoimmune diseases, septic shock, blood clot, stroke, fever, acute respiratory distress syndrome (ARDS) and cachexia. The present sequence is an ARE-mRNA shown in the exemplification of the invention.

XX Sequence 17 BP; 5 A; 0 C; 0 G; 12 U; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. NO. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1590 AAATATATAAACTAAAT 1605
||||| |||||
16 AAATATAATAATAAT 1

RESULT 935

AAL53708/c

ID AAL53708 standard; RNA; 17 BP.

XX AAL53708;

XX 07-FEB-2003 (first entry)

XX Adenylate Uridylate-rich element motif SEQ ID No 2.

XX Target RNA; target RNA:support-attached test compound; flow cytometry; mass spectrometry; high-throughput screening; RNA motif; ss.

XX Homo sapiens.

XX WO200283837-A1.

XX 24-OCT-2002.

XX 11-APR-2002; 2002WO-US11758.

XX 11-APR-2001; 2001US-282966P.

XX (PTCT-) PTC THERAPEUTICS INC.

XX Almstead NG;

XX WPI; 2003-075534/07.

XX Identifying a test compound that binds to a target RNA molecule by separating the detectably labeled target RNA:support-attached test compound complex from uncomplexed target RNA molecules and test compounds by flow cytometry.

XX Disclosure; Page 16; 131pp; English.

The invention relates to a novel method for identifying a test compound that binds to a target RNA molecule comprising separating the detectably labeled target RNA: support-attached test compound complex from uncomplexed target RNA molecules and test compounds. The separating process is carried out by flow cytometry and determining a structure of the type of test compound of the RNA: support-attached test compound complex by mass spectrometry. The method is useful for high-throughput screening of libraries of compounds to identify pharmaceutical leads. This polynucleotide sequence represents one of the target RNA motifs/regions of the invention.

Sequence 17 BP; 5 A; 0 C; 0 G; 12 U; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 8.1e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1590 AAATATATAAGTAAT 1605

||||| | | | | | | | | |

16 AAATAAATAAATAAT 1

RESULT 935

AAZ2707/C

AAA22707 standard; RNA; 17 BP.

AAA22707;

19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SEQ ID NO:5933.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytotaxtic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberculous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

WO9950403-A2.

07-OCT-1999.

24-MAR-1999; 99WO-US06507.

27-MAR-1998; 98US-0079678.

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors

Claim 54; Page 237; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAAL6775 to AAAL7167 and AAAL7561 to AAAL7622 represent ribozyme sequences for ARNT, and AAAL7168 to AAAL7560 and AAAL7623 to AAAL7684 represent their corresponding target sequences; AAAL7685 to AAAL8385 and AAAL9087 to AAAL9154 represent ribozyme sequences for Tie-2, and AAAL9386 to AAAL9086 and AAAL9155 to AAAL9222 represent their corresponding target sequences; AAAL9223 to AAAL20361 and AAAL21501 to AAAL21595 represent ribozyme

sequences for integrin alpha 6 subunit, and AAAL20362 to AAAL21500 and AAAL21596 to AAAL21688 represent their corresponding target sequences; AAAL1689 to AAAL22475 and AAAL23263 to AAAL23342 represent ribozyme sequence for integrin subunit beta 3, and AAAL22476 to AAAL23262, AAAL23343 to AAAL3422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiofibroma of tuberculous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 4 A; 0 C; 0 G; 13 U; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 8.1e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1590 AAATATATAAGTAAT 1605

||||| | | | | | | | | |

16 AAATAAATAAATAAT 1

RESULT 937

ABT37900

ID ABT37900 standard; DNA; 17 BP.

ABT37900;

12-JUN-2003 (first entry)

Tumour suppression related human fukutin oligo SEQ ID NO 3537.

Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sence; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.

Homo sapiens.

WO2003025175-A2.

27-MAR-2003.

17-SEP-2002; 2002WO-IB04208.

17-SEP-2001; 2001FR-0011978.

(MOLE-) MOLECULAR ENGINES LAB.

Telerman A, Amson R, Tuijnder M;

WPI; 2003-313353/30.

New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells

Disclosure; Page 447; 720pp; French.

The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents,

and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention.

Sequence 17 BP; 7 A; 1 C; 1 G; 8 T; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1160 ATTAATGATGTTTAA 1175

|||||
2 ATCAATTTATTTA 17

RESULT 938
AAV96639/C
AAV96639 standard; RNA; 17 BP.

AAV96639;

01-MAR-1999 (first entry)

Potato citrate synthase target sequence position 1333.

Solanidine; glucosyltransferase; potato; citrate synthase; target;
hammerhead ribozyme; hairpin ribozyme; alkaloid biosynthesis;
flower formation; cleavage; solanaceous plant; ss.

Solanum tuberosum.

WO9832843-A2.

30-JUL-1998.

14-JAN-1998; 98WO-US00738.

24-NOV-1997; 97US-0979416.

28-JAN-1997; 97US-0036545.

28-JAN-1997; 97US-0036599.

(RIBO-) RIBOZYME PHARM INC.

McSwiggen JA, Zwick MG;

WPI; 1998-427939/36.

New enzymatic nucleic acid(s) - useful for, e.g. reducing alkaloid biosynthesis or regulating flowering

Claim 53; Page 56; 79pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA-cleaving activity (e.g. ribozymes) which are capable of modulating the expression of plant genes: (i) involved in biosynthesis of alkaloids; or (ii) involved in flower formation. AAV95982 to AAV96334, and AAV96335 to AAV96354 represent potato solanidine glucosyltransferase and hammerhead and hairpin ribozymes, respectively. AAV95629 to AAV95981, and AAV96355 to AAV96734 represent potato solanidine glucosyltransferase target sequences. AAV96773 to AAV97170, and AAV97171 to AAV97195 represent potato citrate synthase hammerhead and hairpin ribozymes, respectively. AAV96735 to AAV96772, and AAV97196 to AAV97220 represent potato citrate synthase target sequences. Ribozymes of the present

invention can be used to inhibit the synthesis of toxic alkaloids in solanaceous plants, particularly potato but also tomato, pepper, aubergine and ditura or to inhibit flowering in potato, lettuce, spinach, cabbage, brussel sprouts, arugula, kale, collards, chard, beet, turnip, sweet potato and turf grass. Also the ribozymes can be used for RNA manipulation in the same way that restriction endonucleases are for DNA, as well as to examine genetic drift and mutations in plants and to detect specific RNA. The ribozymes can be targeted to specific genes or to consensus sequences within a family of related genes, and being catalytic need to be present at only very low concentrations.

Sequence 17 BP; 6 A; 1 C; 3 G; 7 U; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1245 TTCAGATAAACCAACAA 1260

Db 17 TTCAGTTAAACCTTAA 2

RESULT 939

AAA21468

ID AAA21468 standard; RNA; 17 BP.

XX AAA21468;

DT 19-JUN-2000 (first entry)

Integrin alpha 6 subunit substrate sequence SEQ ID NO:4694.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberos sclerosi; dot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

WO9950403-A2.

07-OCT-1999.

24-MAR-1999; 99WO-US06507.

27-MAR-1998; 98US-0079678.

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors

Claim 55; Page 210; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their corresponding target sequences; AAA17685 to AAA18195 and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19155 and AAA19222 represent their corresponding target sequences; AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme

sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT.
 CC Integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus scleriosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 X Q Sequence 17 BP; 9 A; 0 C; 0 G; 8 U; 0 other;
 Query Match 0.9%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 43.8%; Pred. No. 8.1e+02;
 Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 ZY 628 AATAATTTTGAATA 643
 DB 1 AATAAUAUUUUUAUA 16
 RESULT 940
 ID AAA22904 standard; RNA; 17 BP.
 AC AAA22904;
 DT 19-JUN-2000 (first entry)
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6130.
 XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 XX hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 XX age related macular degeneration; inflammation; neovascular glaucoma;
 XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 XX tuberosus scleriosis; pot-wine stain; Sturge Weber syndrome;
 XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 OS
 XX
 XX
 XX WO9950403-A2.
 XX
 XX 07-OCT-1999.
 XX
 XX 24-MAR-1999; 99WO-US06507.
 XX
 XX 27-MAR-1998; 98US-0079678.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX
 XX WPI; 1998-591315/50.
 XX
 XX Novel ribozymes for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding an angiogenic factor -
 XX
 XX Claim 54; Page 249; 305pp; English.
 XX
 XX The present invention describes enzymatic nucleic acid molecules with
 XX RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,

CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT.
 CC Integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus scleriosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 X Q Sequence 17 BP; 12 A; 0 C; 0 G; 5 U; 0 other;
 Query Match 0.9%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 62.5%; Pred. No. 8.1e+02;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 OY 620 AAAACACCAATTAATTT 635
 DB 1 AAUAUAAUAUAUAU 16
 RESULT 941
 ID AAV96640/c standard; RNA; 17 BP.
 XX AAV96640;
 AC AAV96640;
 DT 01-MAR-1999 (first entry)
 DE Potato citrate synthase target sequence position 1334.
 XX Solanidine; glucosyltransferase; potato; citrate synthase; target;
 XX hammerhead ribozyme; hairpin ribozyme; alkaloid biosynthesis;
 XX flower formation; cleavage; solanaceous plant; ss.
 XX Solanum tuberosum.
 OS
 XX WO9832843-A2.
 XX
 XX 30-JUL-1998.
 XX
 XX 14-JAN-1998; 98WO-US00738.
 XX
 XX 24-NOV-1997; 97US-0979416.
 XX
 XX 28-JAN-1997; 97US-0036545.
 XX
 XX 28-JAN-1997; 97US-0036599.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 XX McSwiggen JA, Zwick MG;
 XX
 XX WPI; 1998-427939/36.
 XX
 XX New enzymatic nucleic acid(s) - useful for, e.g. reducing alkaloid
 XX biosynthesis or regulating flowering
 XX
 XX Claim 53; Page 56; 79pp; English.
 XX
 XX The present invention describes enzymatic nucleic acid molecules with
 XX RNA-cleaving activity (e.g. ribozymes) which are capable of modulating
 XX the expression of plant genes: (i) involved in biosynthesis of
 CC alkaloids; or (ii) involved in flower formation. AAV95982 to AAV96334,

and AAV96335 to AAV96354 represent potato solanidine glucosyltransferase hammerhead and hairpin ribozymes, respectively. AAV95629 to AAV95981, and AAV96355 to AAV96734 represent potato solanidine glucosyltransferase target sequences. AAV96773 to AAV97170, and AAV97171 to AAV97195 represent potato citrate synthase hammerhead and hairpin ribozymes, respectively. AAV96735 to AAV96772, and AAV97196 to AAV97220 represent potato citrate synthase target sequences. Ribozymes of the present invention can be used to inhibit the synthesis of toxic alkaloids in solanaceous plants, particularly potato but also tomato, pepper, aubergine and ditura or to inhibit flowering in potato, lettuce, spinach, cabbage, brussel sprouts, arugula, kale, collards, chard, beet, turnip, sweet potato and turf grass. Also the ribozymes can be used for RNA manipulation in the same way that restriction endonucleases are for DNA, as well as to examine genetic drift and mutations in plants and to detect specific RNA. The ribozymes can be targeted to specific genes or to consensus sequences within a family of related genes, and being catalytic need to be present at only very low concentrations.

Sequence 17 BP; 5 A; 1 C; 4 G; 7 U; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1245 TTCAGTAAACAA 1260
|||||
16 TTCAGTTAAACCA 1

SULT 942

AA2896
AA22898 standard; RNA; 17 BP.

AA22898;

19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SEQ ID NO:6124.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiobroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

WO9950403-A2.

07-OCT-1999.

24-MAR-1999; 99WO-US06507.

27-MAR-1998; 98US-0079678.

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts B, Jarvis T, Coeshott C, McSwiggen JA;

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors -

Claim 54; Page 249; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3

gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086 and AAA19155 to AAA19222 represent their corresponding target sequences; AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and AAA21596 to AAA21688 represent their corresponding target sequences; AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequences for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to AAA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiobroma of tuberous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 13 A; 0 C; 0 G; 4 U; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 8.1e+02;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1251 TAAACAAATAAT 1266

Db 1 UAAAAAUAUAUAU 16

RESULT 943

AAA25454

ID AAA25454 standard; DNA; 17 BP.

AC AAA25454;

XX 19-JUN-2000 (first entry)

XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1952.

XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.

XX Homo sapiens.

XX WO9954459-A2.

XX 28-OCT-1999.

XX 19-APR-1999; 99WO-US08547.

XX 20-APR-1998; 98US-0082404.

XX 23-JUN-1998; 98US-0103636.

XX (RIBO-) RIBOZYME PHARM INC.

XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Maebert P;

PI Matulic-Adamic J;

XX WPI; 2000-013248/01.

XX New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer -

PS Claim 77; Page 79; 148pp; English.

C The present invention describes nucleic acids (A) that interact stably
C with a target sequence and contain at least one phosphorodithioate
C link, having endonuclease activity. (A), and more generally any
C catalytic nucleic acid (A') that modulates expression of the oestrogen
C receptor gene, are used to treat cancer (particularly of breast or
C endometrium), in vivo or by transforming cells ex vivo and implanting
C treated cells, or for other conditions associated with levels of
C oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
C can also be used to correlate inhibition of gene expression with
C alterations in phenotype, particularly for identification of therapeutic
C targets, and as research reagents (for RNA, in the same way that
C restriction endonucleases are used with DNA). The combination of
C modifications in (A) improves resistance to nucleases, binding affinity
C and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
C hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
C corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
C receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
C their corresponding target sequences. AAA26219 to AAA26271 represent
C other ribozyme sequences and antisense oligonucleotides used in the
C exemplification of the present invention.

X Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
Q Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Y 1040 TTTATTATTATGAT 1055
b 2 TTTTATTTTGTAT 17

RESULT 945
BK56852/c
ID ABK56852 standard; RNA; 17 BP.
AC ABK56852;
XT 02-JUL-2002 (first entry)
DE Human CLCA1 gene enzymatic nucleic acid #1223.
CW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
CW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
CW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
CW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
CW acetylcysteine.
DS Homo sapiens.
CX WO200211674-A2.
CX 14-FEB-2002.
CX 09-AUG-2001; 2001WO-US24970.
CX 09-AUG-2000; 2000US-224383P.
CX (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTEX USA LLC.
PA (THOM/) THOMPSON J.
XX Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grupe A;
XX WPI; 2002-217145/27.
XX Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma -
PS Claim 4; Page 84; 152pp; English.

CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention.

SQ Sequence 17 BP; 8 A; 4 C; 2 G; 3 U; 0 other;
Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1283 TTTATGTTTATCTGAA 1298
Db 17 TTGTTGTTTCAGCTGAA 2

RESULT 945
ABZ60733/c
ID ABZ60733 standard; RNA; 17 BP.
XX AC ABZ60733;
XX 21-MAR-2003 (first entry)
DS Human K-Ras DNazyme substrate #845.
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
OS Homo sapiens.
PN WO200297114-A2.
XX 05-DEC-2002.
XX 29-MAY-2002; 2002WO-US16840.
XX 29-MAY-2001; 2001US-294140P.
PR 06-JUN-2001; 2001US-296249P.
PR 10-SEP-2001; 2001US-318471P.
XX (RIBO-) RIBOZYME PHARM INC.
PA McSwiggen J;
XX WPI; 2003-140484/13.
XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -
XX Claim 58; Page 101; 185pp; English.
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and
CC anti-rheumatic activity. The nucleic acid molecules are useful for

reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target sequences for the human ribozymes of the invention.

Sequence 17 BP; 9 A; 0 C; 1 G; 7 U; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

623 AACACAAATAATTTT 638
16 AAACTATTATTTT 1

SUIT 946
ABZ61098/c
ABZ61098 standard; RNA; 17 BP.

ABZ61098;

21-MAR-2003 (first entry)

Human K-Ras DNzyme substrate #1210.

Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras; enzymatic nucleic acid; H-Ras; N-Ras; HIV; Cytostatic; anti-HIV; anti-rheumatic; cancer; AIDS; ss.

Homo sapiens.

WO200297114-A2.

05-DEC-2002.

29-MAY-2002; 2002WO-US16840.

29-MAY-2001; 2001US-294140P.

06-JUN-2001; 2001US-296249P.

10-SEP-2001; 2001US-318471P.

(RIBO-) RIBOZYME PHARM INC.

McSwiggen J;

WPI; 2003-140484/13.

Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences -

Claim 58; Page 108; 185pp; English.

The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, ABZ66530 - ABZ66585 represent substrate/target sequences for the human ribozymes of the invention.

Sequence 17 BP; 4 A; 2 C; 3 G; 8 U; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1501 TGCATTTTAAATACA 1516
DB 17 TGCATGTAATAATACA 2

RESULT 947

AAAX74782/c

ID AAX74782 standard; RNA; 17 BP.

XX

AC AAX74782;

XX

DT 28-JUL-1999 (first entry)

DE

Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #310.

XX

Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor; foetal liver kinase 1; ss.

XX

OS Mus sp.

XX

PN WO9715662-A2.

XX

PD 01-MAY-1997.

XX

PP 25-OCT-1996; 96WO-US17480.

XX

PR 11-JAN-1996; 96US-0584040.

XX

PR 26-OCT-1995; 95US-0005974.

XX

PA (CHIR) CHIRON CORP.

XX

PI (RIBO-) RIBOZYME PHARM INC.

XX

EScobedo J, McSwiggen J, Pavco P, Stinchcomb D;

XX

WPI; 1997-259017/23.

XX

Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient

XX

Claim 4; Page 164; 218pp; English.

XX

The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention.

XX

Sequence 17 BP; 11 A; 4 C; 1 G; 1 U; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 8.1e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 464 CTTCATGATGATGCTG 479

DB 16 CTTCATGATGATGCTG 1

RESULT 948

AAAX69088/c

ID AAX69088 standard; RNA; 17 BP.

XX

C AAX69088;
 K 28-JUL-1999 (first entry)
 I Human flt1 VEGF receptor hammerhead ribozyme substrate #383.
 E
 K Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 K flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 K tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 K fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 K foetal liver kinase 1; ss.
 K Homo sapiens.
 S WO9715662-A2.
 K 01-MAY-1997.
 D 25-OCT-1996; 96WO-US17480.
 K 11-JAN-1996; 96US-0584040.
 R 26-OCT-1995; 95US-0005974.
 R (CHIR) CHIRON CORP.
 A (RIBO-) RIBOZYME PHARM INC.
 A
 X Escobedo J, McSwiggen J, Pavco P, Scinchcomb D;
 I WPI; 1997-259017/23.
 R Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 X mRNA stability - useful for treating e.g. tumour angiogenesis,
 T psoriasis, rheumatoid arthritis, etc., in a human patient
 X Claim 4; Page 58; 218pp; English.
 X The present invention describes nucleic acid molecules which modulate
 C the synthesis, expression and/or stability of a mRNA encoding 1 or more
 C receptors of vascular endothelial growth factor (VEGF). A patient
 C (preferably human) having a condition associated with the level of the
 C fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 C receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 C angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 C be treated by administering the nucleic acid molecule or the expression
 C vector to the patient. AAX67275 to AAX75752 represent specific examples
 C of nucleic acid molecules from the present invention.
 X Sequence 17 BP; 11 A; 4 C; 1 G; 1 U; 0 other;
 X
 Query Match 0.9%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 8.1e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Y 464 CTCATGATTTGTTG 479
 D 16 CTCATGATTTGTTG 1
 RESULT 949
 AAX21377/C
 ID AAX21377 standard; RNA; 17 BP.
 K AAX21377;
 AC
 K 19-JUN-2000 (first entry)
 D Integrin alpha 6 subunit substrate sequence SEQ ID NO:4603.
 DE
 X Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 K integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 K hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 K ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 K dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 K

KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberculous scleriosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 OS Homo sapiens.
 XX WO9950403-A2.
 FN 07-OCT-1999.
 PD 24-MAR-1999; 99WO-US06507.
 XX 27-MAR-1998; 98US-0079678.
 PR (RIBO-) RIBOZYME PHARM INC.
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 DR Novel ribozymes for modulating the synthesis, expression and/or
 XX stability of an mRNA encoding an angiogenic factors -
 PT Claim 55; Page 204; 305pp; English.
 XX The present invention describes enzymatic nucleic acid molecules with
 CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAX16775 to
 CC AAX17167 and AAX17561 to AAX17622 represent ribozyme sequences for ARNT,
 CC and AAX17168 to AAX17560 and AAX17623 to AAX17684 represent their
 CC corresponding target sequences; AAX17685 to AAX18385 and AAX19087 to
 CC AAX19154 represent ribozyme sequences for Tie-2, and AAX18386 to AAX19086
 CC and AAX19155 to AAX19222 represent their corresponding target sequences;
 CC AAX19223 to AAX20361 and AAX21501 to AAX21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAX20362 to AAX21500 and
 CC AAX21596 to AAX21688 represent their corresponding target sequences;
 CC AAX21689 to AAX22475 and AAX23263 to AAX23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAX22476 to AAX23262, AAX23343 to
 CC AAX23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3.
 XX Sequence 17 BP; 6 A; 1 C; 1 G; 9 U; 0 other;
 X
 Query Match 0.9%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 8.1e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Y 1251 TAAACCAAAATATT 1266
 D 16 TAAACCAAAATATT 1
 RESULT 950
 AAX74671/C
 ID AAX74671 standard; DNA; 17 BP.
 XX AAX74671;
 AC
 X 24-DEC-2002 (first entry)
 DT Human PAPP-Ea associated 17-mer SEQ ID 197.
 XX

PAPP-E; human; pregnancy associated plasma protein E; abortive;
contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
dysgenetic pregnancy; primer; ss.

Homo sapiens.

US2002102252-A1.

01-AUG-2002.

06-APR-2001; 2001US-0827998.

26-MAY-2000; 2000US-207456P.

(GUY/) GU Y.

(SHAN/) SHANNON M E.

Gu Y, Shannon ME;

WPI; 2002-697817/75.

New isolated nucleic acid encoding an isoform of human pregnancy
associated plasma protein E, for preventing or aborting pregnancy

Example 2; Page 101; 353pp; English.

This invention describes a novel isolated nucleic acid that encodes
one of three new isoforms of human pregnancy associated plasma protein E,
hPAPP-E. The products of the invention have abortive and contraceptive
activity and can be used for gene therapy or in a vaccine. The nucleic
acid, polypeptide encoded by it, or antibody to the polypeptide can be
used in pharmaceutical compositions or vaccines for preventing or
aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
dysgenetic pregnancies. The nucleic acids are used as probes to assess
the level of PAPP-E isoform mRNA in chorionic villus samples, and the
antibodies can be used to assess the expression levels of PAPP-E isoform
proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
antenatally. This sequence represents an oligomer used in scanning the
human PAPP-E genes described in the disclosure of the invention.

Sequence 17 BP; 7 A; 1 C; 1 G; 8 T; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1012 TTATTTCAAGTGTA 1027

||||| |||||

17 TTATTTAAATGCAA 2

RESULT 951

AS74672/C

) ABS74672 standard; DNA; 17 BP.

ABS74672;

24-DEC-2002 (first entry)

Human PAPP-Ea associated 17-mer SEQ ID 198.

PAPP-E; human; pregnancy associated plasma protein E; abortive;
contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
dysgenetic pregnancy; primer; ss.

Homo sapiens.

US2002102252-A1.

01-AUG-2002.

06-APR-2001; 2001US-0827998.

26-MAY-2000; 2000US-207456P.

(GUY/) GU Y.

(SHAN/) SHANNON M E.

Gu Y, Shannon ME;

WPI; 2002-697817/75.

New isolated nucleic acid encoding an isoform of human pregnancy
associated plasma protein E, for preventing or aborting pregnancy

Example 2; Page 101; 353pp; English.

This invention describes a novel isolated nucleic acid that encodes
one of three new isoforms of human pregnancy associated plasma protein E,
hPAPP-E. The products of the invention have abortive and contraceptive
activity and can be used for gene therapy or in a vaccine. The nucleic
acid, polypeptide encoded by it, or antibody to the polypeptide can be
used in pharmaceutical compositions or vaccines for preventing or
aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
dysgenetic pregnancies. The nucleic acids are used as probes to assess
the level of PAPP-E isoform mRNA in chorionic villus samples, and the
antibodies can be used to assess the expression levels of PAPP-E isoform
proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
antenatally. This sequence represents an oligomer used in scanning the
human PAPP-E genes described in the disclosure of the invention.

Sequence 17 BP; 7 A; 1 C; 2 G; 7 T; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1012 TTATTTCAAGTGTA 1027

||||| |||||

16 TTATTTAAATGCAA 1

RESULT 952

ABT36211/C

ID ABT36211 standard; DNA; 17 BP.

ABT36211;

12-JUN-2003 (first entry)

Tumour suppression related human fukutin oligo SEQ ID No 1848.

Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
schizophrenia; protein chip; gene therapy; tumour suppression;
human fukutin; ds.

Homo sapiens.

WO2003025175-A2.

27-MAR-2003.

17-SEP-2002; 2002WO-IB04208.

17-SEP-2001; 2001FR-0011978.

(MOLE-) MOLECULAR ENGINES LAB.

Telerman A, Amson R, Tuljinder M;

WPI; 2003-313353/30.

New isolated nucleic acid, useful for treating viral diseases
associated with tumors and cell degeneration, also related
polypeptides, antibodies and transfected cells

X Disclosure; Page 249; 720pp; French.

X The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterized by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention.

X Sequence 17 BP; 5 A; 2 C; 6 G; 4 T; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 947 CTTACTCAGTGTAT 962
b | | | | | | | | | |
17 CCTACATCAGTGTAT 2

RESULT 953
ABT38326
ID ABT38326 standard; DNA; 17 BP.
AC ABT38326;
XC
X 12-JUN-2003 (first entry)
X Tumour suppression related human fukutin oligo SEQ ID No 3963.
X Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
X antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
X schizophrenia; protein chip; gene therapy; tumour suppression;
X human fukutin; ds.
X Homo sapiens.
X WO2003025175-A2.
X
X 27-MAR-2003.
X
X 17-SEP-2002; 2002WO-IB04208.
X
X 17-SEP-2001; 2001FR-0011978.
X
X (MOLE-) MOLECULAR ENGINES LAB.
X
X Telerman A, Amson R, Tuijnder M;
X WPI; 2003-313353/30.
X
X New isolated nucleic acid, useful for treating viral diseases
X associated with tumors and cell degeneration, also related
X polypeptides, antibodies and transfected cells -
X
X Disclosure; Page 497; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterized by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention.

XX Sequence 17 BP; 8 A; 1 C; 1 G; 7 T; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1613 ATTAAATATATATTT 1628
Db | | | | | | | | | |
2 ATCTTAATATATATTT 17

RESULT 954
AAF79673
ID AAF79673 standard; DNA; 18 BP.
AC AAF79673;
XC
X 29-MAY-2001 (first entry)
X Human Akt-3 antisense oligonucleotide, SEQ ID NO: 81.
X Human; Akt-3; protein kinase; cytostatic; antiinflammatory; infection;
X antisense therapy; inflammation; tumour; ss.
X Homo sapiens.
X US6187586-B1.
X
X 13-FEB-2001.
X
X 29-DEC-1999; 99US-0474922.
X
X 29-DEC-1999; 99US-0474922.
X
X (ISIS-) ISIS PHARM INC.
X Monia BP, Cowseert LM, Roth RA;
X WPI; 2001-264979/27.
X
X New antisense compounds targeting nucleic acids encoding human Akt-3
X useful for treating a disease or condition associated with Akt-3
X expression, or in preventing or delaying inflammation or tumor
X formation -
X
X Claim 1; Column 40; 37pp; English.
X
X The present sequence is one of a number of antisense compounds of up to
X 30 nucleobases in length targeted to a nucleic acid encoding human Akt-3.

The antisense compounds are useful for inhibiting the expression of human Akt-3 in human cells or tissues. They are also useful for modulating the expression of Akt-3, and for treating a human or an animal suspected of having, or being prone to, a disease or condition associated with Akt-3 expression. The antisense compounds may also be used as research reagents, in kits and in diagnostics, e.g. to elucidate the function of a particular gene or to distinguish between functions of various members of a biological pathway; and as a prophylactic, e.g. to prevent or delay infection, inflammation or tumour formation.

Sequence 18 BP; 3 A; 3 C; 1 G; 11 T; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 8.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1555 TCTCCAAATTTTCTTT 1570
|||||
3 TCTCATATTTCTTT 18

RESULT 955
X37761
AA337761 standard; DNA; 18 BP.

AA337761;

09-JUL-1999 (first entry)

Staphylococcus sp. detecting oligonucleotide fsg2s.

FemA; primer; identification; detection; therapy; infection; femB; amplification; genotyping; gram-positive bacteria; vaccine; ss.

Synthetic.

Staphylococcus sp.

WC9916780-A2.

08-APR-1999.

28-SEP-1998; 98WO-BE00141.

26-SEP-1997; 97EP-0870146.

(BENA-) BELGIAN MIN NAT DEFENCE.

(UYLO-) UNIV CATHOLIQUE LOUVAIN.

Gala J, Vanmuffel P;

WPI; 1999-287521/24.

New Staphylococcus-specific oligonucleotides

Claim 5; Page 8; 48pp; English.

This invention describes novel Staphylococcus-specific oligonucleotides based on the consensus femA nucleotide sequence which are used to develop products for the identification, detection and therapy of infections. The oligonucleotides can be used for the genetic amplification, the identification and/or quantification of various femA sequences which are specific to known or unknown Staphylococci species. Since the femA sequence is similar to the femB sequence, the oligonucleotides can also be used for the molecular genotyping of femB. Genes of different Staphylococci species or other gram-positive bacteria. The femA nucleic acids can also be used in therapeutic applications. They can also be used to identify inhibitors, e.g. antibodies or antisense oligonucleotides, for blocking expression of the femA nucleotide sequences. They can also be used for producing vaccines against Staphylococci infections.

Sequence 18 BP; 12 A; 1 C; 3 G; 2 T; 0 other;

Query Match 0.9%; Score 11.2; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 8.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 619 AAAACAACTAAT 634
|||||
DB 1 AAAAGTACAAAAAT 16

RESULT 956
ABK34044/c
ID ABK34044 standard; DNA; 18 BP.

XX ABK34044;

DT 18-JUN-2002 (first entry)

DE Human NF1 probe #2.

XX Human; ss; astrocytoma; cytostatic; staging; cysteine methylation; CpG; bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry; matrix assisted laser desorption/ionization mass spectrometry; probe.

XX Homo sapiens.

PN WO200202808-A2.

PD 10-JAN-2002.

PF 02-JUL-2001; 2001WO-BP07538.

PR 30-JUN-2000; 2000DE-1032529.

PR 01-SEP-2000; 2000DE-1043826.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-171649/22.

PT Novel chemically modified genomic DNA sequences, useful in the characterisation, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas or predisposition to astrocytomas

Example 2; Page 18; 37pp; English.

The invention relates to a nucleic acid comprising a sequence (I) of at least 18 bases in length of a segment of chemically pre-treated genomic DNA which has any one of the sequences of (ABK33919-ABK34032) or its complement. Also included are an oligonucleotide or peptide nucleic acid (or set thereof) of at least 9 nucleotides which hybridises to (I), primers for (I), probes for detecting cytosine methylation or single-nucleotide polymorphisms (SNP) in (I), an array of oligomers or peptide nucleic acids for analysing diseases associated with the methylation states of the CpG dinucleotides of (I). The array is useful for determining genetic and/or epigenetic parameters. Classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas, or the predisposition to astrocytomas by analysing cytosine methylation, involves obtaining a biological sample containing genomic DNA, extracting the genomic DNA, converting cytosine bases which are unmethylated at the 5-position, in the genomic DNA sample, to uracil or another base which is dissimilar to cytosine in terms of hybridisation behaviour, by chemical treatment and amplifying chemically pre-treated genomic DNA fragments using the array and a polymerase, where the amplification carries a detectable label. The method further involves identifying methylation status of one or more cytosine positions, and analysing methylation status of the cytosine positions by reference to one or more data sets. The genomic DNA is chemically treated by using a bisulphite, hydrogen sulphite or disulphite. The amplification step amplifies DNA which is of particular interest in astrocytoma or brain tissue, based on the specific genomic methylation status of brain tissues, as opposed to background DNA. The amplification carries a

fluorescent label or radionuclide. Optionally, the labels of the amplicates are detachable molecule fragments having a typical mass which are detected in a mass spectrometer. The fragments of chemically pre-treated genomic DNA to be amplified, have a single positive or negative charge for a better detectability in the mass spectrometer. Preferably, the amplicates or fragments of the amplicates are detected by matrix assisted laser desorption/ionization mass spectrometry (MALDI) or using electron spray mass spectrometry (ESI). The present sequence is a probe used to detect a region containing a methylated cytosine from one of the chemically pre-treated reference DNA samples of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 18 BP; 11 A; 4 C; 0 G; 3 T; 0 other;
Query Match 0.9%; Score 11.2; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 8.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1535 TTTAGATCTTTTAT 1550
17 TTTAGGGTGTTTAAT 2

RESULT 957
AD37308
D AAD37308 standard; DNA; 19 BP.
X C AAD37308;
X T 21-AUG-2002 (first entry)
X 3' primer #5 used for selective amplification of human ARE mRNAs.
X Human; untranslated region; UTR; adenylate uridylylate-rich element; ARE;
X cancer; gene expression; PCR; primer; ss.
X Homo sapiens.
X WO2001:83691-A2.
X 08-NOV-2001.
X 12-APR-2001; 2001WO-US11993.
X 12-APR-2000; 2000US-196870P.
X (CLEV-) CLEVELAND CLINIC FOUND.
X (KING-) KING FAISAL SPECIALIST HOSPITAL & RES CE.
X Abu-Khabar KS, Williams BRG, Prevel M, Silverman RH;
X WPI; 2002-055473/07.
X Selecting adenylate uridylylate-rich element (ARE) coding sequences from
X databases, comprises extracting nucleic acids with protein coding
X sequences upstream, contiguous with a 3' untranslated region having a
X specific ARE sequence -
X Disclosure; Page 12; 106pp; English.

The invention relates to a gene discovery system and gene expression systems specific for genes encoding adenylate uridylylate-rich element (ARE)-containing mRNAs. The invention relates to a method of selecting nucleic acids which involves extracting protein coding sequences from a database which contains several nucleic acids, each of which comprises full-length or partial protein coding sequences and a 3' untranslated region (UTR) sequence downstream and contiguous with protein coding sequences by identifying protein coding sequences located upstream and contiguous with a 3' UTR which has an adenylate uridylylate-rich element

(ARE) search sequence. The method is used for selecting a set of nucleic acids for analysing gene expression in a cell. Nucleic acids of the invention are useful for preparing a customised array of ARE genes. The microarrays produced are useful for obtaining an ARE expression profile in a subject. The microarrays are useful for obtaining an ARE expression profile, particularly a subject with a disease such as cancer. The ARE genes identified by the above mentioned method are useful for generation of polymerase chain reaction (PCR) products or oligonucleotides for use as immobilised probes in cDNA or oligonucleotide microarrays. The present sequence is a PCR primer which is used for the selective amplification of human ARE mRNAs by reverse transcription.

Sequence 19 BP; 14 A; 0 C; 0 G; 5 T; 0 other;
Query Match 0.9%; Score 11.2; DB 1; Length 19;
Best Local Similarity 81.2%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1591 AATATAAAGTAATA 1606
1 AATAATAAATAATA 16

RESULT 958
AAH90994/C
ID AAH90994 standard; DNA; 19 BP.
X AC AAH90994;
X 09-OCT-2001 (first entry)
X Human inflammatory bowel disease associated polymorphic site #69.
X Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
X single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
X chromosome 5q31-33; forensic test; gene therapy; ds.
X Homo sapiens.
X Key Location/Qualifiers
X misc_feature 11
X /tag= a
X /note= "SNP, optionally A or T at this position"

WO200142511-A2.
14-JUN-2001.
11-DEC-2000; 2000WO-US33632.
10-DEC-1999; 99US-0170257.
10-APR-2000; 2000US-0196046.
(WHED) WHITEHEAD INST BIOMEDICAL RES.
(ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
WPI; 2001-367874/38.
Testing for the presence of polymorphisms associated with inflammatory bowel disease, using a hybridization assay -
Claim 1; Page 42; 463pp; English.

The present invention describes a method for detecting the presence of polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease states. They may be used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a polymorphic site described in the exemplification of the invention.


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} Sequence 19 BP; 5 A; 0 C; 1 G; 12 T; 1 other;
Query Match 0.9%; Score 11.2; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

622 AACACAAATTAATTTT 638
|||||
19 AAAAAAATTAATTTT 3

SULT 959
I54044
AAL54044 standard; DNA; 24 BP.
AAL54044;
06-MAR-2003 (first entry)
Human macroprotein 16-39 PCR primer 1.
Human macroprotein 16.39; embryotic development deformity; tumour;
DNA recombination; PCR; primer; ss.
Homo sapiens.
CNI342711-A.
03-APR-2002.
12-SEP-2000; 2000CN-0125188.
12-SEP-2000; 2000CN-0125188.
(BODE-) BODE GENE DEV CO LTD SHANGHAI.
Mao Y, Xie Y;
WPI; 2002-529786/57.
Polypeptide-human macroprotein 16.39 and polynucleotide for coding it -
Example 2; Page 19 (Disclosure); 35pp; Chinese.
The invention relates to the novel human macroprotein 16.39. The
invention also relates to the polynucleotide for coding the protein, the
process for preparing the protein by DNA recombination technique, the
application of the protein in treating several diseases such as embryotic
development deformity and tumours, the antagonist against this protein
and its therapeutic action, and the application of the polynucleotide
coding this new human macroprotein 16.35. This polynucleotide sequence
represents a PCR primer of the human macroprotein 16.39 of the invention.
Sequence 24 BP; 7 A; 2 C; 2 G; 13 T; 0 other;
Query Match 0.9%; Score 11.2; DB 1; Length 24;
Best Local Similarity 66.7%; Pred. No. 8.9e+02;
Matches 16; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

1137 AGTAAATTAATTTTATTTAGATA 1160
|||||
1 AGCATTAATTAATTTTATTTAGATA 24

SULT 960
BF53002/c
ABF53002 standard; DNA; 13 BP.
ABF53002;
21-FEB-2002 (first entry)

DE XX Oligonucleotide SEQ ID NO 152999 for detecting SNP TSC0038671.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX PD
XX 06-APR-2001; 2001WO-IB00713.
XX 07-APR-2000; 2000DE-1019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-557177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
XX Claim 1; SEQ ID 152999; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 4 A; 0 C; 0 G; 8 T; 1 other;
Query Match 0.9%; Score 11; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 7.4e+02;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1613 ATTTAAATATATA 1625
DB 13 RTTAAATATATA 1

RESULT 961
ABF53003
ID ABF53003 standard; DNA; 13 BP.
XX
AC ABF53003;
XX
DT 21-FEB-2002 (first entry)
XX
DE XX Oligonucleotide SEQ ID NO 153000 for detecting SNP TSC0038671.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX PD
XX 06-APR-2001; 2001WO-IB00713.
XX
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X R 07-APR-2000; 2000DE-1019173.
 X A (EPIC-) EPICENOMICS AG.
 X I Olek A, Piepenbrock C, Berlin K;
 X R WPI; 2001-657177/75.
 X T Set of oligonucleotides, useful for diagnosis and cell typing, is
 T designed to detect single nucleotide polymorphisms and cytosine
 T methylation status
 X S Claim 1; SEQ ID 153000; 29pp + Sequence Listing; German.
 X C This invention describes novel oligonucleotide primers or peptide nucleic
 C acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 C and cytosine methylation status in chemically pretreated genomic DNA. The
 C oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 C range of diseases including immune system, gastrointestinal, respiratory,
 C central nervous system, cardiovascular and metabolic disorders. The
 C oligomers are also used for detecting cell type differentiation.
 C AB000010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and
 C AB100010-AB182073 represent the oligomers described in the invention.
 C NOTE: The sequence data for this patent did not form part of the printed
 C specification, but was obtained in electronic format from WIPO at
 C ftp.wipo.int/pub/published_pct_sequences.
 X Q Sequence 13 BP; 8 A; 0 C; 0 G; 4 T; 1 other;
 Query Match 0.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 7.4e+02;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Y 1613 ATTAAATATATA 1625
 Y 1 RTTAAATATATA 13
 RESULT 962
 AAT81506
 ID AAT81506 standard; RNA; 17 BP.
 AC AAT81506;
 CX AAT81506;
 EX 14-DEC-1997 (first entry)
 DE Human c-myb hammerhead ribozyme target sequence (nt. position 2713).
 DE Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;
 DE smooth muscle cell; hyperproliferation; restenosis; cancer;
 DE c-myb; coronary angioplasty; ss.
 OS Homo sapiens.
 XX WO9531541-A2.
 XX 23-NOV-1995.
 XX 18-MAY-1995; 95WO-US06368.
 XX 13-JAN-1995; 95US-0373124.
 XX 18-MAY-1994; 94US-0245466.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Draper K, Jarvis T, McSwiggen J, Stinchcomb DT;
 XX WPI; 1996-010927/01.
 XX New enzymatic nucleic acid molecules - which cleave RNA produced by
 XX e.g. c-myb, for treating restenosis or cancer
 Claim 1; Page 77; 128pp; English.
 The present sequence represents the preferred target sequence for an
 enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 the human c-myb sequence at the base position indicated in the
 descriptor line. The c-myb sequence was screened for optimal ribozyme
 target sites using a computer folding algorithm, and regions of the mRNA
 which did not form secondary folding structures and contained potential
 ribozyme cleavage sites were identified. Ribozymes were synthesised and
 their activities optimised by either varying the length of the binding
 arms or by modification to prevent degradation by nucleases.
 The ribozymes cleave the c-myb sequence and can be used to prevent
 smooth muscle cell hyperproliferation in restenosis, especially after
 coronary angioplasty, and in cancers.

PS Claim 1; Page 77; 128pp; English.
 XX The present sequence represents the preferred target sequence for an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the human c-myb sequence at the base position indicated in the
 CC descriptor line. The c-myb sequence was screened for optimal ribozyme
 CC target sites using a computer folding algorithm, and regions of the mRNA
 CC which did not form secondary folding structures and contained potential
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised and
 CC their activities optimised by either varying the length of the binding
 CC arms or by modification to prevent degradation by nucleases.
 CC The ribozymes cleave the c-myb sequence and can be used to prevent
 CC smooth muscle cell hyperproliferation in restenosis, especially after
 CC coronary angioplasty, and in cancers.
 XX SQ Sequence 17 BP; 9 A; 0 C; 0 G; 8 U; 0 other;
 Query Match 0.9%; Score 11; DB 1; Length 17;
 Best Local Similarity 27.3%; Pred. No. 8.7e+02;
 Matches 3; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
 QY 1522 TTATATTTTAA 1532
 Db 7 UUAUUAUUUUA 17
 RESULT 963
 AAT81507
 ID AAT81507 standard; RNA; 17 BP.
 AC AAT81507;
 CX AAT81507;
 DT 14-DEC-1997 (first entry)
 DE Human c-myb hammerhead ribozyme target sequence (nt. position 2715).
 DE Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;
 DE smooth muscle cell; hyperproliferation; restenosis; cancer;
 DE c-myb; coronary angioplasty; ss.
 OS Homo sapiens.
 XX WO9531541-A2.
 XX 23-NOV-1995.
 XX 18-MAY-1995; 95WO-US06368.
 XX 13-JAN-1995; 95US-0373124.
 XX 18-MAY-1994; 94US-0245466.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Draper K, Jarvis T, McSwiggen J, Stinchcomb DT;
 XX WPI; 1996-010927/01.
 XX New enzymatic nucleic acid molecules - which cleave RNA produced by
 XX e.g. c-myb, for treating restenosis or cancer
 Claim 1; Page 77; 128pp; English.
 The present sequence represents the preferred target sequence for an
 enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 the human c-myb sequence at the base position indicated in the
 descriptor line. The c-myb sequence was screened for optimal ribozyme
 target sites using a computer folding algorithm, and regions of the mRNA
 which did not form secondary folding structures and contained potential
 ribozyme cleavage sites were identified. Ribozymes were synthesised and
 their activities optimised by either varying the length of the binding
 arms or by modification to prevent degradation by nucleases.
 The ribozymes cleave the c-myb sequence and can be used to prevent
 smooth muscle cell hyperproliferation in restenosis, especially after

coronary angioplasty, and in cancers.
Sequence 17 BP; 7 A; 0 C; 0 G; 10 U; 0 other;
Query Match 0.9%; Score 11; DB 1; Length 17;
Best Local Similarity 27.3%; Pred. No. 8.7e+02;
Matches 3; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
1522 TTAATTTTGA 1532
5 UUAUUAUUUA 15
RESULT 964
AAV24553/c
AAV24553 standard; DNA; 17 BP.
AAV24553;
16-SEP-1998 (first entry)
PCR primer for DNA polymerase fragment coding sequence.
DNA polymerase; HBV; RNA intermediate; nucleotide analogue sensitivity;
surface antigen interaction; sAg; antibody interaction; PCR primer;
anti-viral therapy; ss.
Synthetic.
Hepatitis b virus.
WO9821317-A1.
22-MAY-1998.
15-AUG-1997; 97WO-AU00520.
08-NOV-1996; 96AU-0003519.
(WHEA-) WESTERN HEALTH CARE NETWORK.
Aye TT, Bartholomeusz AI, De Man RA, Locarnini SA;
WPI; 1998-297924/26.
Variants of DNA virus replicating through RNA intermediate,
especially hepatitis B - have mutations in genes for DNA polymerase,
surface antigen or region of overlapping reading frames, and show
reduced sensitivity to antiviral agents or antibodies
Example 3; Page 19; 53pp; English.
This sequence is a PCR primer for DNA encoding a fragment of a
Hepatitis b virus (HBV) DNA polymerase. The amplified fragment can be
mutated to give the variant of a DNA virus of the invention, that
replicates via an RNA intermediate. Detection of mutations in the
encoded protein sequence can be used in a method for determining if a HBV
isolate has reduced sensitivity to a nucleotide analogue or if its
surface antigen (sAg) has reduced interaction with antibodies. Mutations
in the DNA polymerase gene indicate (partial) resistance to nucleotide
analogues while those in the sAg gene indicate reduced interaction with
specific antibodies. Detecting sequences containing these mutations is
used to monitor anti-viral treatments (chemotherapy and/or vaccination)
and to screen for agents that can overcome the effects of such mutations
(potentially useful in long-term treatments with nucleotide analogues).
Sequence 17 BP; 5 A; 4 C; 1 G; 7 T; 0 other;
Query Match 0.9%; Score 11; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1081 AAGAAATTGGA 1091
|||||||

Db 13 AAGAAATTGGA 3
RESULT 965
AAV24555/c
AAV24555 standard; DNA; 17 BP.
XX AAV24555;
XX AAV24555;
DT 16-SEP-1998 (first entry)
XX PCR primer for DNA polymerase fragment coding sequence.
XX DNA polymerase; HBV; RNA intermediate; nucleotide analogue sensitivity;
KW surface antigen interaction; sAg; antibody interaction; PCR primer;
KW anti-viral therapy; ss.
XX Synthetic.
OS Hepatitis b virus.
OS WO9821317-A1.
PN 22-MAY-1998.
PD 15-AUG-1997; 97WO-AU00520.
XX 08-NOV-1996; 96AU-0003519.
XX (WHEA-) WESTERN HEALTH CARE NETWORK.
PA Aye TT, Bartholomeusz AI, De Man RA, Locarnini SA;
XX WPI; 1998-297924/26.
XX Variants of DNA virus replicating through RNA intermediate,
PT especially hepatitis B - have mutations in genes for DNA polymerase,
PT surface antigen or region of overlapping reading frames, and show
PT reduced sensitivity to antiviral agents or antibodies
XX Example 3; Page 19; 53pp; English.
XX This sequence is a PCR primer for DNA encoding a fragment of a
XX Hepatitis b virus (HBV) DNA polymerase. The amplified fragment can be
XX mutated to give the variant of a DNA virus of the invention, that
XX replicates via an RNA intermediate. Detection of mutations in the
XX encoded protein sequence can be used in a method for determining if a HBV
XX isolate has reduced sensitivity to a nucleotide analogue or if its
XX surface antigen (sAg) has reduced interaction with antibodies. Mutations
XX in the DNA polymerase gene indicate (partial) resistance to nucleotide
XX analogues while those in the sAg gene indicate reduced interaction with
XX specific antibodies. Detecting sequences containing these mutations is
XX used to monitor anti-viral treatments (chemotherapy and/or vaccination)
XX and to screen for agents that can overcome the effects of such mutations
XX (potentially useful in long-term treatments with nucleotide analogues).
XX Sequence 17 BP; 5 A; 4 C; 1 G; 7 T; 0 other;
Query Match 0.9%; Score 11; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1081 AAGAAATTGGA 1091
|||||||
Db 13 AAGAAATTGGA 3
RESULT 966
AAV71403/c
AAV71403 standard; DNA; 17 BP.
XX AAV71403;
XX AAV71403;
DT 25-MAR-2003 (updated)

T 18-APR-1991 (first entry)
 X Sequence of hybridization probe to detect the H. grisea
 E glucoamylase gene based on GAL peptide.
 F
 W Enzyme; fungal expression vector; Aspergillus expression vector;
 W Trichoderma; ss.
 X Humicola grisea.
 S
 N BP215594-A.
 X
 X 25-MAR-1987.
 D
 X 27-AUG-1986; 86EP-0306624.
 F
 X 29-AUG-1985; 85US-0771374.
 R
 R 29-AUG-1985; 85US-0771394.
 R
 R 07-JUL-1986; 86US-0882224.
 X
 A (GEMV) GENENCOR INC.
 X
 X Cullen D, Gray GL, Hayenga KJ, Lawlis VB;
 I WPI; 1987-095049/14.
 R
 X New DNA sequences for expressing polypeptide in filamentous fungi
 T - with secretion of prod. from the cells, and new vectors and
 T transformed fungi
 T
 X Example; Fig 20; 45pp; English.
 S
 X A DNA sequence coding for a heterologous polypeptide which can be
 C expressed in and secreted from filamentous fungi is claimed. Pref.
 C the DNA sequence codes for bovine preprochymosin, M. meinel
 C preprocarboxyl protease or A. niger preproglucoamylase. Also new
 C are vectors consisting of the DNA sequence plus an operably-linked
 C signal sequence. The vectors may also include a sequence which
 C increases transformation efficiency, e.g. ANS-1.
 C (Updated on 25-MAR-2003 to correct PR field.)
 C (Updated on 25-MAR-2003 to correct PA field.)
 X
 X Sequence 17 BP; 8 A; 1 C; 0 G; 3 T; 5 other;
 Q

Query Match 0.9%; Score 11; DB 1; Length 17;
 Best Local Similarity 69.2%; Pred. No. 8.7e+02;
 Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1047 TTTATGATTTAT 1059
 ||:|:|:|:|:|:
 Db 17 TTATRTATTTT 5

RESULT 967
 AAQ78885/C
 ID AAQ78885 standard; DNA; 17 BP.
 AC AAQ78885;
 X
 X 25-MAR-2003 (updated)
 X 18-DEC-1995 (first entry)
 X
 X Humicola grisea glucoamylase hybridization probe.
 X
 X Glucoamylase; DNA probe; gene cloning; protein secretion; ss.
 X Synthetic.
 X EP25577-A1.
 X
 X 23-NOV-1994.
 X
 X 27-AUG-1986; 94EP-0201751.

XX 29-AUG-1985; 85US-0771374.
 PR 07-JUL-1986; 86US-0882224.
 PR 27-AUG-1986; 86EP-0306624.
 XX
 PA (GEMV) GENENCOR INT INC.
 XX
 X Berka RM, Cullen D, Gray GL, Hayenga KJ, Lawlis VB;
 FI WPI; 1994-359750/45.
 XX
 DR
 XX
 XX Vectors and DNA for expressing polypeptide(s) in filamentous fungi
 PT - include secretory signal sequences that are native or foreign to
 PT heterologous polypeptide(s), such as chymosin or glucoamylase.
 X
 XX Example 9A3; Page 22; 50pp; English.
 PS
 XX The DNA probe and corresponding probes covering the degenerate
 CC sites (AAQ7886-Q78891) correspond to amino acids 17-22 of the
 CC H. grisea glucoamylase peptide GAL (AAR62933), and are used as
 CC hybridization probes to detect and isolate H. grisea glucoamylase
 CC DNA in a Southern blot. Resulting genomic DNA fragments are
 CC excised and cloned in plasmid pRS1. This illustrates the main
 CC claims of the patent, i.e. a vector containing (i) DNA encoding
 CC a heterologous polypeptide (chymosin, prochymosin, preprochymosin,
 CC Aspergillus niger glucoamylase, H. grisea glucoamylase, or Mucor
 CC miehei carboxyl protease) and (ii) a secretory signal peptide,
 CC and a filamentous fungus (Aspergillus, Trichoderma, Neurospora,
 CC Podospora, Endothia, Mucor, Cochliobolus or Pyricularia, especially
 CC A. nidulans, A. awamori or T. reesei) transformed with the vector
 CC for recombinant protein (enzyme) production.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 X
 X Sequence 17 BP; 8 A; 1 C; 0 G; 3 T; 5 other;
 SQ

Query Match 0.9%; Score 11; DB 1; Length 17;
 Best Local Similarity 69.2%; Pred. No. 8.7e+02;
 Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1047 TTTATGATTTAT 1059
 ||:|:|:|:|:|:
 Db 17 TTATRTATTTT 5

RESULT 968
 AAV44676
 ID AAV44676 standard; DNA; 20 BP.
 XX
 AC AAV44676;
 X
 X 08-OCT-1998 (first entry)
 X
 X PCR primer for UC Band#325-1.
 X
 X DNA marker; metastatic prostate cancer; human; detection; PCR primer;
 X disease marker identification; lupus erythematosus; rheumatoid arthritis;
 X multiple sclerosis; asthma; myasthenia gravis; autoimmune thyroiditis;
 X amyloid lateral sclerosis; interstitial cystitis; prostatitis;
 X UC Band#325-1; ss.
 X Synthetic.
 OS Homo sapiens.
 XX WO9824935-A1.
 X
 X 11-JUN-1998.
 X
 X 05-DEC-1997; 97WO-US22105.
 X
 X 24-MAR-1997; 97US-0041576.
 X 06-DEC-1996; 96US-0032619.
 X 12-DEC-1996; 96US-0032701.

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X (UROC-) UROCOR INC.
X An G, O'Hara M, Ralph D, Veltri R;
X WPI; 1998-333350/29.
X Identifying markers for disease states - by amplifying RNA from
X peripheral blood and identifying RNA which is differential expressed
X between normal and disease state subjects
X Example 3; Page 91; 158pp; English.
X This sequence is a PCR primer for the marker DNA sequence UC Band#325-1
X and was used in the method of the invention. The method is for
X identifying markers for a disease state, and comprises: (a) providing a
X first set of peripheral blood mRNAs from one or more subjects known to
X exhibit the disease state and a second set of peripheral blood mRNAs from
X one or more normal subjects; (b) amplifying both sets of mRNAs to provide
X nucleic acid amplification products; (c) comparing the sets of
X differentially expressed between normal subjects and subjects exhibiting
X the disease state; and (d) identifying those mRNAs that are
X differentially expressed between normal subjects and subjects exhibiting
X the disease state; where a difference in quantity of expression of an
X mRNA is indicative of a disease marker. The identified marker
X sequence can be used in a method of detecting a metastatic cancer disease
X state, especially for detection prostate cancer. Using the methods, a
X disease state may be detected, diagnosed, or a prognosis may be delivered
X by examining a blood sample rather than relying on a more invasive, or
X less sensitive test. In addition, a subject may be monitored for disease
X progression, status and response to therapies through monitoring of
X differentially expressed disease markers. The methods can be used for
X diseases such as cancer (especially metastatic or prostate cancer),
X asthma, lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
X myasthenia gravis, autoimmune thyroiditis, amyloid lateral sclerosis,
X interstitial cystitis, prostatitis or other systemic or chronic conditions.
X Sequence 20 BP; 7 A; 8 C; 3 G; 2 T; 0 other;
Query Match 0.9%; Score 11; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 850 TGGCAACCCCTA 860
b 1 TGGCAACCCCTA 11
RESULT 969
AV44678
D AAV44678 standard; DNA; 20 BP.
X AAV44678;
X 08-OCT-1998 (first entry)
X PCR primer for UC Band#325-2.
X DNA marker; metastatic prostate cancer; human; detection; PCR primer;
X disease marker identification; lupus erythematosus; rheumatoid arthritis;
X multiple sclerosis; asthma; myasthenia gravis; autoimmune thyroiditis;
X amyloid lateral sclerosis; interstitial cystitis; prostatitis;
X UC Band#325-2; ss.
X Synthetic.
X Homo sapiens.
X WO9824935-A1.
X 11-JUN-1998.
X 05-DEC-1997; 97WO-US22105.
X 24-MAR-1997; 97US-0041576.

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PR 06-DEC-1996; 96US-0032619.
PR 12-DEC-1996; 96US-0032701.
PR (UROC-) UROCOR INC.
XX An G, O'Hara M, Ralph D, Veltri R;
XX WPI; 1998-333350/29.
XX Identifying markers for disease states - by amplifying RNA from
XX peripheral blood and identifying RNA which is differential expressed
XX between normal and disease state subjects
XX Example 3; Page 91; 158pp; English.
XX This sequence is a PCR primer for the marker DNA sequence UC Band#325-2
XX and was used in the method of the invention. The method is for
XX identifying markers for a disease state, and comprises: (a) providing a
XX first set of peripheral blood mRNAs from one or more subjects known to
XX exhibit the disease state and a second set of peripheral blood mRNAs from
XX one or more normal subjects; (b) amplifying both sets of mRNAs to provide
XX nucleic acid amplification products; (c) comparing the sets of
XX differentially expressed between normal subjects and subjects exhibiting
XX the disease state; and (d) identifying those mRNAs that are
XX differentially expressed between normal subjects and subjects exhibiting
XX the disease state; where a difference in quantity of expression of an
XX mRNA is indicative of a disease marker. The identified marker
XX sequence can be used in a method of detecting a metastatic cancer disease
XX state, especially for detection prostate cancer. Using the methods, a
XX disease state may be detected, diagnosed, or a prognosis may be delivered
XX by examining a blood sample rather than relying on a more invasive, or
XX less sensitive test. In addition, a subject may be monitored for disease
XX progression, status and response to therapies through monitoring of
XX differentially expressed disease markers. The methods can be used for
XX diseases such as cancer (especially metastatic or prostate cancer),
XX asthma, lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
XX myasthenia gravis, autoimmune thyroiditis, amyloid lateral sclerosis,
XX interstitial cystitis, prostatitis or other systemic or chronic conditions.
XX Sequence 20 BP; 7 A; 8 C; 3 G; 2 T; 0 other;
Query Match 0.9%; Score 11; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 850 TGGCAACCCCTA 860
Db 1 TGGCAACCCCTA 11
RESULT 970
AAZ30727
ID AAZ30727 standard; DNA; 20 BP.
XX AAZ30727;
XX 19-JAN-2000 (first entry)
XX Human interleukin-8 (IL-8) RT-PCR primer #11.
XX Interleukin-8; IL-8; marker; expression; diagnosis;
XX differential; disease; cancer; metastatic; breast cancer; prostate;
XX peripheral leukocyte; immune response; asthma; lupus erythematosus;
XX rheumatoid arthritis; multiple sclerosis; myasthenia gravis;
XX autoimmune thyroiditis; amyotrophic lateral sclerosis; ALS;
XX interstitial cystitis; prostatitis; mRNA; reverse transcriptase PCR;
XX RT-PCR; screening; early; diagnosis; prognosis; monitoring; primer; ss.
XX Synthetic.
XX Homo sapiens.
XX WO9949083-A1.
XX 30-SEP-1999.

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X F 24-MAR-1999; 99WO-US06488.
X R 24-MAR-1998; 98US-0046894.
X A (UROC-) UROC INC.
X I Ralph D, An G, O'Hara SM, Veltri RW;
X R WPI; 1999-591105/50.
X T Identifying markers of human disease, specifically for diagnosis of
X T metastatic prostatic and breast cancers -
X S Example 3; Page 122; 225pp; English.
X C This sequence represents human interleukin-8 (IL-8) reverse
C transcriptase-PCR (RT-PCR) primer #11, used with primers #10 (AAZ30726)
C or #12 (AAZ30728) to amplify 2 different IL-8 cDNAs (AAZ30714-Z30715)
C from peripheral leukocyte RNA. IL-8 cDNA is referred to in this
C specification as UC Band #325-1, while an IL-8 cDNA containing intron #3
C is referred to as UC Band #325-2. The IL-8 gene was found to be
C differentially expressed between healthy subjects and patients with
C metastatic cancers (especially those of the prostate or breast) and may
C therefore be used as a marker for such diseases. Detecting levels of such
C human disease markers is used for diagnosis (also prognosis and
C monitoring) of diseases, including metastatic or organ-confined cancers,
C and diseases which also elicit an immune response such as asthma, lupus
C erythematosus, rheumatoid arthritis, multiple sclerosis, myasthenia
C gravis, autoimmune thyroiditis, amyotrophic lateral sclerosis (ALS),
C interstitial cystitis and prostatitis. A particular use is differentiating between
C prostatic cancer and benign prostatic hypertrophy, and between advanced
C and localised prostatic cancer, by multivariate analysis of several
C different markers. Cancers can be treated by administering sequences
C antisense to sequences that encode human disease markers. This method
C detects a leukocyte response to disease rather than products of diseased
C cells, so is suitable for large-scale screening of asymptomatic subjects.
C Disease can be detected at an early stage, when few, if any, diseased
C cells are present in the circulation. Analysis of blood samples
C eliminates the need for more invasive methods for obtaining samples.
X Q Sequence 20 BP; 7 A; 8 C; 3 G; 2 T; 0 other;
Query Match 0.9%; Score 11; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
JY 850 TGGCAACCCCTA 860
DB 1 TGGCAACCCCTA 11
RESULT 971
ID AAS21760/c
AC AAS21760 standard; DNA; 20 BP.
AC AAS21760;
DT 21-NOV-2001 (first entry)
DE Mouse Survivin antisense oligonucleotide #62.
KW Survivin; human; mouse; cytosolic; antisense oligonucleotide;
KW hyperproliferative condition; cancer; apoptosis; cytokinesis; ss.
OS Mus musculus.
OS Synthetic.
FN WO200157059-A1.
XX 09-AUG-2001.
XX

PF 30-JAN-2001; 2001WO-US02939.
PR XX
XX 02-FEB-2000; 2000US-0496694.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Ackermann EJ, Swayze SE, Cowseert LM;
XX DR WPI; 2001-488863/53.
XX PT Novel antisense compounds for modulating the expression of Survivin and
XX PS treatment of cancer -
XX PS Example 18; Page 62; 120pp; English.
XX CC The invention relates to antisense oligonucleotides targeted to a nucleic
CC acid molecule encoding human Survivin, where the antisense
CC oligonucleotide inhibits the expression of human Survivin. These
CC antisense oligonucleotides are used in the treatment of an animal
CC suffering from a disease or condition associated with Survivin, e.g. a
CC hyperproliferative condition such as cancer, and comprises administering
CC a therapeutically or prophylactically effective amount of the antisense
CC oligonucleotide so that expression of Survivin is inhibited. The
CC oligonucleotides can also be used to treat a human suffering from a
CC disease or condition characterised by a reduction in apoptosis
CC comprising administering the antisense oligonucleotide to a human. In
CC addition, the antisense oligonucleotide and a cytotoxic chemotherapeutic
CC agent e.g. taxol or cisplatin, can be used to modulate apoptosis,
CC cytokinesis or the cell cycle, or inhibit the proliferation in a cancer
CC cell by contacting the cell with the antisense oligonucleotide.
CC AAS21521-AAS21768 represent Survivin nucleic acids, and antisense
CC oligonucleotides targeted to Survivin, used in the method of the
CC invention.
XX SQ Sequence 20 BP; 6 A; 0 C; 2 G; 12 T; 0 other;
Query Match 0.9%; Score 11; DB 1; Length 20;
Best Local Similarity 73.7%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1250 ATAAACACACAAATTAATTTT 1268
DB 19 ATACAAAATAATAACTTT 1
RESULT 972
ID AAH80901
AC AAH80901 standard; cDNA; 20 BP.
XX AC AAH80901;
XX DT 19-SEP-2001 (first entry)
XX DE Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 865.
XX KW Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
XX KW disease diagnosis; ss.
XX OS Human immunodeficiency virus type 1.
XX XX US6251588-B1.
XX PD 26-JUN-2001.
XX XX 10-FEB-1998; 98US-0021701.
XX XX 10-FEB-1998; 98US-0021701.
XX PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX WPI; 2001-424456/45.
XX DR

K Predicting the potential of an oligonucleotide to hybridize to a target
 I nucleotide sequence, useful for evaluating oligonucleotide probe
 F sequences, by identifying a oligonucleotides based on the evaluation of
 D parameters

{ Example 2; Column 73; 342pp; English.

{ The present invention describes a method for predicting the potential of
 { an oligonucleotide to hybridize to a (complementary) target nucleotide
 { sequence, involving identifying a subset of oligonucleotides within the
 { predetermined number of unique oligonucleotides based on the evaluation
 { of the parameter. Oligonucleotides in the subset are identified that are
 { clustered along a region of the nucleotide sequence that is hybridisable
 { to the target nucleotide sequence. This is useful for evaluating
 { oligonucleotide probe sequences. The present sequence is an
 { oligonucleotide described in the exemplification of the invention.

{ Sequence 20 BP; 9 A; 1 C; 5 G; 5 T; 0 other;

Query Match 0.9%; Score 11; DB 1; Length 20;
 Best Local Similarity 73.7%; Pred. No. 9.2e+02;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

518 TCGTAAATTTGCAATTCA 536
 |||||
 2 TCGGAAATTTAAAGTGCA 20

RESULT 973

10Q79313/C
 AAQ79313 standard; DNA; 21 BP.

AAQ79313;

25-MAR-2003 (updated)

23-JUN-1995 (first entry)

Human c-raf-1 oncogene mRNA 2819-2798 antisense oligonucleotide DK-23.

Antisense oligonucleotide; ras-activated cancer cells;
 anti-raf-1 oncogene; antisense inhibition of translation; ss.

Synthetic.

WO9423755-A1.

27-OCT-1994.

11-APR-1994; 94WO-US04091.

09-APR-1993; 93US-0045374.

(OYNE-) UNIV NEBRASKA.

Iversen PL;

WPI; 1994-341496/42.

New heterotypic anti-raf antisense oligonucleotide(s) - for
 killing ras-activated cancer cells.

Disclosure; Page 61; 81pp; English.

Anti-raf antisense oligonucleotides can be used to kill cancer cells
 which contain an activated ras oncogene. This is one of a group of
 antisense oligonucleotides which are exemplified in the
 specification; they are 8-50 nucleotides long and are antisense to
 regions of the A-raf-1 or the c-raf-1 genes obtained from the
 "HUGENE" gene library.

(Updated on 25-MAR-2003 to correct PN field.)

Sequence 21 BP; 14 A; 6 C; 0 G; 1 T; 0 other;

Query Match 0.9%; Score 11; DB 1; Length 21;
 Best Local Similarity 73.7%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1043 ATTATTATGTAATTATT 1061
 |||||
 Db 20 ATTGTTGTTGTTAGTT 2

RESULT 974

AAH62202

ID AAH62202 standard; DNA; 21 BP.

XX

AC

AAH62202;

XX

DT

12-SEP-2001 (first entry)

XX

DE

Per tyrosine kinase polymorphism containing DNA fragment #103.

XX

KW

Single nucleotide polymorphism; SNP; human; cancer; inflammation;

KW

heart disease; paternity testing; forensic science; ds.

XX

OS

Homo sapiens.

XX

Key

Location/Qualifiers

Variation

replace(11.G)

/*tag= a

FT

/standard_name= "single nucleotide polymorphism"

XX

PN

WO200138576-A2.

XX

PD

31-MAY-2001.

XX

PF

17-NOV-2000; 2000WO-US31639.

XX

PR

24-NOV-1999; 99US-0167334.

XX

PA

(WHED) WHITEHEAD INST BIOMEDICAL RES.

XX

PI

Cargill M, Ireland JS, Lander ES;

XX

DR

WPI; 2001-367705/38.

XX

PT

New nucleic acid segments of the human genome, particularly from genes

XX

PT

including polymorphic sites, for phenotype correlation, forensics,

XX

PT

paternity testing, medicine and genetic analysis -

Claim 1; Page 38; 80pp; English.

DNA sequences AAH62100 - AAH62688 represent segments of human genes which
 contain single nucleotide polymorphisms (SNPs). A method is included in
 the invention for analysing a nucleic acid sample, which consists of
 determining the base occupying any one of the polymorphic sites given in
 the SNP containing sequences. The nucleotide sequences can be used in the
 diagnosis or monitoring of diseases, such as cancer, inflammation, heart
 diseases, diseases of the cardiovascular system, and infection by
 microorganisms. The oligonucleotides are also useful in the manufacture
 of a medicament for the treatment or prophylaxis of the diseases, and as
 applications such as phenotype correlation, forensics, paternity testing,
 medicine and genetic analysis.

Sequence 21 BP; 11 A; 1 C; 4 G; 5 T; 0 other;

Query Match 0.9%; Score 11; DB 1; Length 21;
 Best Local Similarity 73.7%; Pred. No. 9.3e+02;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1597 TCGAATATATAAAGTAAAT 1605
 |||||
 Db 1 TCGAATATATAAAGTAAAT 19

RESULT 975
 E200185/c
 D ABZ00185 standard; DNA; 50 BP.
 X C C ABZ00185;
 X T 09-JAN-2003 (first entry)
 X E Human leukocyte gene expression profiling probe SEQ ID NO 176.
 X T7; leukocyte; gene expression profiling; allograft rejection;
 W atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 W rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection;
 W probe; ss.
 X S Homo sapiens.
 X N WO200257414-A2.
 X D 25-JUL-2002.
 X F 22-OCT-2001; 2001WO-US47856.
 X R 20-OCT-2000; 2000US-241994P.
 X R 08-JUN-2001; 2001US-296764P.
 X A (BIOC-) BIOCARDIA INC.
 X I Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
 X I Ly N, Woodward R, Quertemous T, Johnson F;
 X R WPI; 2002-636525/68.
 X T New system for leukocyte expression profiling, diagnosing a disease, or
 T monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 T or congestive heart failure, comprises diagnostic oligonucleotides
 X S Claim 1; Page 332; 2038pp; English.
 X C The invention relates to a system for detecting gene expression, which
 C comprises one or two isolated DNA molecules that detect expression of a
 C gene, where the gene corresponds to any of 8143 oligonucleotides
 C (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
 C for leukocyte expression profiling. It is particularly useful for
 C diagnosing a disease, monitoring (rate of) progression of a disease,
 C predicting therapeutic outcome, determining prognosis for a patient,
 C predicting disease complications in an individual or monitoring response
 C to treatment in an individual. The diseases include cardiac allograft
 C rejection, kidney allograft rejection, liver allograft rejection,
 C atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 C rheumatoid arthritis, osteoarthritis or cytomegalovirus infection.
 X Q Sequence 50 BP; 14 A; 4 C; 15 G; 17 T; 0 other;
 Query Match 0.9%; Score 11; DB 1; Length 50;
 Best Local Similarity 57.1%; Pred. No. 5.6e+02;
 Matches 20; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 Y 596 AGTATTATTATTGATCTACAAAACACACAAA 630
 b 38 ATTATTCGTAATTACACAGCACTACACACACA 4
 RESULT 976
 UAT56320/c
 D AAT56320 standard; RNA; 15 BP.
 X C AAT56320;
 X T 25-MAR-2003 (updated)
 X T 14-MAY-1997 (first entry)

DE Mouse TNF-a hammerhead ribozyme target sequence (nt position 1310).
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; Interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW Philadelphia chromosome; inflammation; autoimmunity disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.
 OS Mus musculus.
 XX NO9523225-A2.
 XX 31-AUG-1995.
 XX 23-FEB-1995; 95WO-IB00156.
 XX 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 15-APR-1994; 94US-0228041.
 PR 18-MAY-1994; 94US-0245736.
 PR 06-JUL-1994; 94US-0271280.
 PR 15-AUG-1994; 94US-0291932.
 PR 16-AUG-1994; 94US-0291433.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 08-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 23-SEP-1994; 94US-0311749.
 PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.
 PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334847.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpaisky A, Kisich K, Matulic-adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;
 PI Thompson JD, Tracz D, Usman N, Wincott FE, Woolf T;
 WPI; 1995-351090/45.
 DR Ribozymes having modified bases and methods for producing them
 XX for use in inhibiting disease related genes
 PT Claim 2; Page 352; 407pp; English.
 XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC Regions of the mRNA that do not form secondary folding
 CC structures and that contain potential hammerhead and hairpin
 CC ribozyme cleavage sites were identified by computer analysis.
 CC Ribozymes directed against these mRNA sequences were designed and
 CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit TNF-alpha expression, making them

potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as for treatment of AIDS.
(Updated on 25-MAR-2003 to correct PI field.)

Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;

Query Match 0.9%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 8.8e+02; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1250 ATAAACACAAATA 1263

|||||
14 ATAAATATATAATA 1

RESULT 977

AF55811/c

AAT55811 standard; RNA; 15 BP.

AAT55811;

25-MAR-2003 (updated)

25-MAR-1997 (first entry)

Human TNF-alpha hammerhead ribozyme target sequence (nt position 1269).

Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS; ss.

Homo sapiens.

WO9523225-A2.

31-AUG-1995.

23-FEB-1995; 95WO-IB00156.

30-JAN-1995; 95US-0380734.

23-FEB-1994; 94US-0201109.

23-MAR-1994; 94US-0218934.

04-APR-1994; 94US-0222795.

07-APR-1994; 94US-0224483.

15-APR-1994; 94US-0227958.

15-APR-1994; 94US-0228041.

18-MAY-1994; 94US-0245736.

06-JUL-1994; 94US-0271280.

15-AUG-1994; 94US-0291932.

16-AUG-1994; 94US-0291433.

17-AUG-1994; 94US-0292620.

19-AUG-1994; 94US-0293520.

02-SEP-1994; 94US-0300000.

08-SEP-1994; 94US-0303039.

23-SEP-1994; 94US-0311486.

23-SEP-1994; 94US-0311749.

28-SEP-1994; 94US-0314597.

03-OCT-1994; 94US-0316771.

07-OCT-1994; 94US-0319492.

11-OCT-1994; 94US-0321993.

04-NOV-1994; 94US-0334847.

10-NOV-1994; 94US-0337608.

28-NOV-1994; 94US-0345516.

16-DEC-1994; 94US-0357577.

23-DEC-1994; 94US-0363233.

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(RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Chowira B, Dorenzo A, Draper KG, Dudycz LW;

Grimm S, Karpeisky A, Kisch K, Matulic-adamic J, Mcswiggen JA;

Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;

Thompson JD, Tracz D, Usman N, Wincott PE, Woolf T;

WPI; 1995-351090/45.

Ribozymes having modified bases and methods for producing them for use in inhibiting disease related genes

Claim 2; Page 243; 407pp; English.

The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit TNF-alpha expression, making them potentially useful for treating rheumatoid arthritis, septic shock and other inflammatory disorders including psoriasis, as well as for treatment of AIDS.

(Updated on 25-MAR-2003 to correct PI field.)

Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;

Query Match 0.9%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 8.8e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1250 ATAAACACAAATA 1263

|||||
14 ATAAATATATAATA 1

RESULT 978

AAT55796/c

AAT55796 standard; RNA; 15 BP.

AAT55796;

25-MAR-2003 (updated)

25-MAR-1997 (first entry)

Human TNF-alpha hammerhead ribozyme target sequence (nt position 1258).

Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS; ss.

Homo sapiens.

WO9523225-A2.

31-AUG-1995.

23-FEB-1995; 95WO-IB00156.

30-JAN-1995; 95US-0380734.

C resistance. The ribozymes are designed to cleave the target
C sequences and thereby inhibit TNF-alpha expression, making them
C potentially useful for treating rheumatoid arthritis, septic shock
C and other inflammatory disorders including psoriasis, as well as
C for treatment of AIDS.

C (Updated on 25-MAR-2003 to correct PI field.)

C Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;

Query Match 0.9%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 8.8e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1251 TAAACACAAATATA 1264

|||||

15 TAAATATAATATA 2

RESULT 980

VT55809/c

AAT55809 standard; RNA; 15 BP.

AAT55809;

25-MAR-2003 (updated)

25-MAR-1997 (first entry)

Human TNF-alpha hammerhead ribozyme target sequence (nt position 1267).

Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
intercellular adhesion molecule; rel A; tumour necrosis factor;
TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
translocation; chronic myelogenous leukaemia; CML; cancer;
Philadelphia chromosome; inflammation; autoimmune disease;
atherosclerosis; myocardial infarction; stroke; restenosis;
transplant rejection; rheumatoid arthritis; psoriasis;
myocardial ischaemia; Kawasaki disease; septic shock; HIV;
human immunodeficiency virus; acquired immune deficiency syndrome;
AIDS; ss.

Homo sapiens.

WO9523225-A2.

31-AUG-1995.

23-FEB-1995; 95WO-IB00156.

30-JAN-1995; 95US-0380734.

23-FEB-1994; 94US-0201109.

29-MAR-1994; 94US-0218934.

04-APR-1994; 94US-0222795.

07-APR-1994; 94US-0224483.

15-APR-1994; 94US-0227958.

15-APR-1994; 94US-0228041.

18-MAY-1994; 94US-0245736.

06-JUL-1994; 94US-0271280.

15-AUG-1994; 94US-0291932.

16-AUG-1994; 94US-0291433.

17-AUG-1994; 94US-0292620.

19-AUG-1994; 94US-0293520.

02-SEP-1994; 94US-0300000.

08-SEP-1994; 94US-0303039.

23-SEP-1994; 94US-0311486.

23-SEP-1994; 94US-0311749.

28-SEP-1994; 94US-0314337.

03-OCT-1994; 94US-0316771.

11-OCT-1994; 94US-0319492.

04-NOV-1994; 94US-0321993.

10-NOV-1994; 94US-0334847.

28-NOV-1994; 94US-0337608.

94US-0345516.

PR 16-DEC-1994; 94US-0357577.

PR 23-DEC-1994; 94US-0363233.

XX (RIBO-) RIBOZYME PHARM INC.

PI Stinchcomb DT, Chowrira B, Dorenzo A, Draper KG, Dudycz LM;

PI Grimm S, Karpeisky A, Kisich K, Matulic-adamic J, Mcawiggen JA;

PI Kodak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D;

PI Thompson JB, Tracz D, Usman N, Wincott PE, Woolf T;

XX WPI; 1995-351090/45.

XX Ribozymes having modified bases and methods for producing them

XX for use in inhibiting disease related genes

PT Claim 2; Page 243; 407pp; English.

XX The present sequence represents a preferred target sequence for an

CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha

CC mRNA at the nucleotide base position indicated in the DE line.

CC Regions of the mRNA that do not form secondary folding

CC structures and that contain potential hammerhead and hairpin

CC ribozyme cleavage sites were identified by computer analysis.

CC Ribozymes directed against these mRNA sequences were designed and

CC synthesised with modifications that improve their nuclease

CC resistance. The ribozymes are designed to cleave the target

CC sequences and thereby inhibit TNF-alpha expression, making them

CC potentially useful for treating rheumatoid arthritis, septic shock

CC and other inflammatory disorders including psoriasis, as well as

CC for treatment of AIDS.

CC (Updated on 25-MAR-2003 to correct PI field.)

CC Sequence 15 BP; 4 A; 0 C; 0 G; 11 U; 0 other;

XX Query Match 0.9%; Score 10.8; DB 1; Length 15;

XX Best Local Similarity 85.7%; Pred. No. 8.8e+02;

XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 TAAACACAAATATA 1264

|||||

15 TAAATATAATATA 2

Db

RESULT 981

AAF70070/c

ID AAF70070 standard; DNA; 15 BP.

XX AC AAF70070;

XX 18-APR-2001 (first entry)

DT Human TNFRSF1B gene ASO probe, SEQ ID NO: 126.

DE Human; TNFRSF1B; osteoclastogenesis inhibitory factor;

XX single nucleotide polymorphism; SNP; osteoclast recruitment;

XX osteoclast function; osteoporosis; metastatic bone disease;

XX Paget's disease; rheumatoid arthritis; periodontal bone disease;

XX ASO; allele-specific oligonucleotide; probe; ss.

OS Homo sapiens.

WO200104137-A1.

PN 18-JAN-2001.

PD 10-JUL-2000; 2000WO-US18803.

PF 09-JUL-1999; 99US-0143020.

PR (GENA-) GENAISSANCE PHARM INC.

PA Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;

XX

Search completed: December 18, 2003, 07:20:29
Job time : 19 secs

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Query Match      0.9%; Score 10.8; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 8.8e+02;
Matches 6: Conservative 6; Mismatches 2; Indels 0; Gaps 0;
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1 UAUAUAUAAU 14

Z3.9954

AAZ39954:

Human interleukin-2 RNA probe L550A.

Synthetic.

JP11285386-A.

03-APR-1998:

(BUNS-) BUNSHI BIOHOTOINICS KENKYUSHO KK.

Detection of the higher-order structure of an RNA - by hybridising with a specific probe

This sequence represents a probe for human interleukin-2 (IL-2) RNA. The invention relates to a method for the detection of the higher-order structure of an RNA, consisting of: (i) reacting the RNA with a probe (P1) having a base sequence (B1) hybridisable with A1 among the specific continuous base sequences A1 and A2 in the RNA and a probe (P2) having a base sequence (B2) hybridisable with A2 among a specific continuous base sequences A1 and A2 in the RNA; (2) detecting the continuous base sequences B1 and B2 formed by hybridising the probes P1 and P2 on the RNA; and (3) judging that: (i) the higher-order structure of the specific continuous base sequences A1 and A2 in the RNA is single-stranded when sequences B1 and B2 are detected; or (ii) the higher-order structure of the specific continuous base sequences A1 and A2 in the RNA is double-stranded when sequences B1 and B2 are not detected. The method can also detect a change in the higher-order structure of an RNA.

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Query Match      0.9%; Score 10.8; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 8.8e+02;
Matches 12: Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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1 | AATAATTAAANTAAA 15

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

M nucleic - nucleic search, using sw model

un on: December 18, 2003, 07:23:37 ; Search time 10 seconds
(without alignments)
2.527 Million cell updates/sec

title: us-09-960-143-3
effect score: 1249
sequence: 1 aaaaattcattctgtggt.....atataattgttgcagaagt 1249

coring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

sarched: 603 seqs, 10117 residues

otal number of hits satisfying chosen parameters: 1206

inimum DB seq length: 8

aximum DB seq length: 50

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 732 summaries

atabase : rni.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

%

result No.	Score	Query Match	Length	DB ID	Description
c 1	24	1.9	24	1	US-09-710-200-72 Sequence 72, Appl
c 2	24	1.9	24	1	US-09-975-408-72 Sequence 72, Appl
c 3	21	1.7	21	1	US-08-246-855A-16 Sequence 16, Appl
c 4	21	1.7	21	1	PCT-US95-07748A-7 Sequence 16, Appl
c 5	20	1.6	20	1	US-09-046-894-11 Sequence 11, Appl
c 6	17.4	1.4	20	1	US-09-165-868-8 Sequence 8, Appl
c 7	16.4	1.3	20	1	US-09-433-694-61 Sequence 61, Appl
c 8	16.2	1.3	22	1	US-08-619-542B-58 Sequence 58, Appl
c 9	15.8	1.3	20	1	US-09-422-978-7355 Sequence 7355, Ap
c 10	15.6	1.2	22	1	US-08-123-449A-1 Sequence 1, Appl
c 11	15.6	1.2	22	1	US-08-123-449A-2 Sequence 2, Appl
c 12	15.6	1.2	22	1	US-08-458-050-1 Sequence 1, Appl
c 13	15.6	1.2	22	1	US-08-458-050-2 Sequence 2, Appl
c 14	15.6	1.2	22	1	US-08-950-196-1 Sequence 1, Appl
c 15	15.6	1.2	22	1	US-08-950-196-2 Sequence 2, Appl
c 16	15.4	1.2	17	1	US-08-146-421-9 Sequence 9, Appl
c 17	15.4	1.2	18	1	US-09-205-144-43 Sequence 43, Appl
c 18	15.4	1.2	20	1	US-09-488-744A-83 Sequence 83, Appl
c 19	15.4	1.2	22	1	US-08-943-731-521 Sequence 521, App
c 20	15.2	1.2	20	1	US-07-322-723A-29 Sequence 29, Appl
c 21	15.2	1.2	20	1	US-07-799-828C-29 Sequence 29, Appl
c 22	15.2	1.2	20	1	US-07-952-277A-29 Sequence 29, Appl
c 23	15.2	1.2	20	1	US-08-780-173A-92 Sequence 92, Appl
c 24	15.2	1.2	21	1	US-08-377-687-53 Sequence 53, Appl
c 25	15.2	1.2	21	1	US-08-777-192-53 Sequence 53, Appl
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c 27	14.8	1.2	20	1	US-09-357-073-33 Sequence 33, Appl
c 28	14.8	1.2	20	1	US-09-280-805-239 Sequence 239, App
c 29	14.8	1.2	20	1	US-09-496-694B-239 Sequence 239, App
c 30	14.8	1.2	20	1	US-09-496-694B-240 Sequence 240, App
c 31	14.8	1.2	20	1	US-09-658-687A-26 Sequence 26, Appl
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c 33	14.8	1.2	21	1	US-08-719-124-7 Sequence 7, Appl

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1	US-08-973-137-7	Sequence 7, Appli
1	US-08-973-137-8	Sequence 8, Appli

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108	13.8	1.1	19	1	US-08-973-137-10	Sequence 10, Appl	181	13.2	1.1	18	1	US-09-144-367-29	Sequence 29, Appl
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110	13.8	1.1	19	1	US-08-973-137-14	Sequence 14, Appl	183	13.2	1.1	18	1	US-09-422-978-5436	Sequence 5436, Ap
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112	13.8	1.1	19	1	US-08-973-137-16	Sequence 16, Appl	185	13.2	1.1	18	1	PCT-US95-08604-92	Sequence 92, Appl
113	13.8	1.1	19	1	US-09-422-978-8817	Sequence 8817, Ap	186	13.2	1.1	14	1	US-08-435-605A-48	Sequence 48, Appl
114	13.8	1.1	19	1	PCT-US93-02259-7	Sequence 7, Appl	187	13	1.0	14	1	US-08-882-649A-9	Sequence 9, Appl
115	13.8	1.1	19	1	PCT-US93-02259-8	Sequence 8, Appl	188	13	1.0	15	1	US-08-334-847-510	Sequence 510, App
116	13.8	1.1	19	1	PCT-US96-08320-1	Sequence 1, Appl	189	13	1.0	15	1	US-08-311-486C-188	Sequence 188, App
117	13.8	1.1	19	1	PCT-US96-08320-1	Sequence 1, Appl	190	13	1.0	15	1	US-08-311-486C-196	Sequence 196, App
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119	13.6	1.1	22	1	US-08-123-449A-2	Sequence 2, Appl	192	13	1.0	15	1	US-08-311-486C-720	Sequence 720, App
120	13.6	1.1	22	1	US-08-458-050-1	Sequence 2, Appl	193	13	1.0	17	1	US-08-311-486C-770	Sequence 770, App
121	13.6	1.1	22	1	US-08-458-050-2	Sequence 2, Appl	194	13	1.0	17	1	US-07-977-284A-168	Sequence 168, App
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128	13.4	1.1	15	1	US-08-311-486C-191	Sequence 191, App	201	13	1.0	17	1	US-08-985-162-517	Sequence 517, App
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137	13.4	1.1	15	1	US-08-311-486C-712	Sequence 712, App	210	12.8	1.0	17	1	US-08-435-628-2037	Sequence 2037, Ap
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139	13.4	1.1	15	1	US-08-311-486C-714	Sequence 714, App	212	12.8	1.0	17	1	US-08-435-628-2153	Sequence 2153, Ap
140	13.4	1.1	15	1	US-08-311-486C-715	Sequence 715, App	213	12.8	1.0	17	1	US-08-435-628-2155	Sequence 2155, Ap
141	13.4	1.1	15	1	US-08-311-486C-716	Sequence 716, App	214	12.8	1.0	17	1	US-08-527-060-23	Sequence 23, Appl
142	13.4	1.1	15	1	US-08-311-486C-721	Sequence 721, App	215	12.8	1.0	17	1	US-08-527-060-23	Sequence 23, Appl
143	13.4	1.1	15	1	US-08-500-635A-13	Sequence 13, Appl	216	12.8	1.0	17	1	US-08-252-620A-1983	Sequence 1983, Ap
144	13.4	1.1	15	1	US-08-682-423-6	Sequence 6, Appl	217	12.8	1.0	17	1	US-09-067-773-29	Sequence 29, Appl
145	13.4	1.1	15	1	US-08-682-423-21	Sequence 21, Appl	218	12.8	1.0	17	1	US-08-988-706-17	Sequence 17, Appl
146	13.4	1.1	15	1	US-09-157-151-13	Sequence 13, Appl	219	12.8	1.0	17	1	US-08-988-706-18	Sequence 18, Appl
147	13.4	1.1	15	1	PCT-US95-05141-6	Sequence 6, Appl	220	12.8	1.0	17	1	US-09-071-845-1983	Sequence 1983, Ap
148	13.4	1.1	15	1	PCT-US95-05141-21	Sequence 21, Appl	221	12.8	1.0	17	1	US-08-584-040-2166	Sequence 2166, Ap
149	13.4	1.1	16	1	US-08-242-402-7	Sequence 7, Appl	222	12.8	1.0	17	1	US-08-584-040-2556	Sequence 2556, Ap
150	13.4	1.1	16	1	US-08-242-402-12	Sequence 12, Appl	223	12.8	1.0	17	1	US-08-584-040-2557	Sequence 2557, Ap
151	13.4	1.1	16	1	US-08-682-423-25	Sequence 25, Appl	224	12.8	1.0	17	1	US-08-584-040-2828	Sequence 2828, Ap
152	13.4	1.1	16	1	US-08-682-423-25	Sequence 25, Appl	225	12.8	1.0	17	1	US-08-584-040-3850	Sequence 3850, Ap
153	13.4	1.1	16	1	PCT-US95-05141-22	Sequence 22, Appl	226	12.8	1.0	17	1	US-08-584-040-4225	Sequence 4225, Ap
154	13.4	1.1	16	1	PCT-US95-05141-25	Sequence 25, Appl	227	12.8	1.0	17	1	US-08-584-040-4226	Sequence 4226, Ap
155	13.4	1.1	17	1	US-08-281-940-54	Sequence 54, Appl	228	12.8	1.0	17	1	US-08-306-420C-4	Sequence 4, Appl
156	13.4	1.1	17	1	US-08-373-124A-970	Sequence 970, App	229	12.8	1.0	17	1	US-08-306-420C-4	Sequence 4, Appl
157	13.4	1.1	17	1	US-08-373-124A-2051	Sequence 2051, App	230	12.8	1.0	17	1	US-08-311-772B-711	Sequence 711, App
158	13.4	1.1	17	1	US-08-435-628-2051	Sequence 2051, App	231	12.8	1.0	17	1	US-08-311-772B-1080	Sequence 1080, Ap
159	13.4	1.1	17	1	US-08-710-134-54	Sequence 54, Appl	232	12.8	1.0	17	1	US-08-311-772B-1081	Sequence 1081, Ap
160	13.4	1.1	17	1	US-08-485-885-54	Sequence 54, Appl	233	12.8	1.0	17	1	US-08-311-772B-1352	Sequence 1352, Ap
161	13.4	1.1	17	1	US-08-584-040-2299	Sequence 2299, Ap	234	12.8	1.0	17	1	US-08-311-772B-1617	Sequence 1617, Ap
162	13.4	1.1	17	1	US-08-584-040-2785	Sequence 2785, Ap	235	12.8	1.0	17	1	US-08-311-772B-1617	Sequence 1617, Ap
163	13.4	1.1	17	1	US-08-584-040-7818	Sequence 7818, Ap	236	12.8	1.0	17	1	US-08-311-772B-1992	Sequence 1992, Ap
164	13.4	1.1	17	1	US-08-584-040-7818	Sequence 7818, Ap	237	12.8	1.0	17	1	US-08-311-772B-1992	Sequence 1992, Ap
165	13.4	1.1	17	1	US-09-371-772B-844	Sequence 844, App	238	12.8	1.0	17	1	US-08-311-772B-4747	Sequence 4747, Ap
166	13.4	1.1	17	1	US-09-371-772B-1309	Sequence 1309, App	239	12.8	1.0	17	1	US-08-311-772B-4747	Sequence 4747, Ap
167	13.4	1.1	17	1	US-09-371-772B-3602	Sequence 3602, App	240	12.8	1.0	17	1	US-08-311-772B-5267	Sequence 5267, Ap
168	13.4	1.1	17	1	US-09-371-772B-5228	Sequence 5228, App	241	12.8	1.0	17	1	US-08-311-772B-5267	Sequence 5267, Ap
169	13.4	1.1	17	1	US-09-371-772B-5584	Sequence 5584, App	242	12.8	1.0	17	1	US-08-311-772B-6945	Sequence 6945, Ap
170	13.4	1.1	18	1	US-09-213-768-31	Sequence 31, Appl	243	12.8	1.0	17	1	US-08-867-941-37	Sequence 37, Appl
171	13.4	1.1	18	1	US-09-315-083-22	Sequence 22, Appl	244	12.8	1.0	18	1	US-08-200-141-22	Sequence 22, Appl
172	13.4	1.1	18	1	US-09-315-083-22	Sequence 22, Appl	245	12.8	1.0	18	1	US-08-319-964-42	Sequence 42, Appl
173	13.4	1.1	18	1	US-08-222-177A-345	Sequence 345, App	246	12.8	1.0	18	1	US-08-319-964-42	Sequence 42, Appl
174	13.4	1.1	19	1	US-08-466-551-8	Sequence 8, Appl	247	12.8	1.0	18	1	US-08-319-964-47	Sequence 47, Appl
175	13.4	1.1	19	1	US-08-422-978-4969	Sequence 4969, Ap	248	12.8	1.0	18	1	US-08-319-964-47	Sequence 47, Appl
176	13.4	1.1	19	1	US-08-271-942A-92	Sequence 92, Appl	249	12.8	1.0	18	1	US-08-745-455A-15	Sequence 15, Appl
177	13.2	1.1	18	1	US-08-779-916A-92	Sequence 92, Appl	250	12.8	1.0	18	1	US-08-745-455A-16	Sequence 16, Appl
178	13.2	1.1	18	1	US-09-474-922A-81	Sequence 81, Appl	251	12.8	1.0	18	1	US-09-425-233-12	Sequence 12, Appl
179	13.2	1.1	18	1	US-09-637-751A-6	Sequence 6, Appl	252	12.8	1.0	18	1	US-09-319-588C-35	Sequence 35, Appl
												US-09-319-588C-91	Sequence 91, Appl

253	12.8	1.0	18	1	US-09-422-978-5250	Sequence 5250, Ap	C 326	12.2	1.0	17	1	US-08-373-124A-962	Sequence 962, App
254	12.8	1.0	18	1	US-09-422-978-6086	Sequence 6086, Ap	C 327	12.2	1.0	17	1	US-08-373-124A-1048	Sequence 1048, Ap
255	12.6	1.0	17	1	US-09-468-265-20	Sequence 20, Appl	C 328	12.2	1.0	17	1	US-08-373-124A-1048	Sequence 1048, Ap
256	12.4	1.0	14	1	US-08-645-789A-4	Sequence 4, Appl	C 329	12.2	1.0	17	1	US-08-373-124A-1058	Sequence 1058, Ap
257	12.4	1.0	14	1	US-08-645-789A-79	Sequence 79, Appl	C 330	12.2	1.0	17	1	US-08-373-124A-1871	Sequence 1871, Ap
258	12.4	1.0	14	1	US-08-617-010C-14	Sequence 14, Appl	C 331	12.2	1.0	17	1	US-08-373-124A-1885	Sequence 1885, Ap
259	12.4	1.0	14	1	US-09-565-591-14	Sequence 14, Appl	C 332	12.2	1.0	17	1	US-08-373-124A-1901	Sequence 1901, Ap
260	12.4	1.0	14	1	US-09-053-832-37	Sequence 37, Appl	C 333	12.2	1.0	17	1	US-08-373-124A-1983	Sequence 1983, Ap
261	12.4	1.0	14	1	US-08-743-481A-24	Sequence 24, Appl	C 334	12.2	1.0	17	1	US-08-373-124A-2147	Sequence 2147, Ap
262	12.4	1.0	14	1	US-09-640-953-37	Sequence 37, Appl	C 335	12.2	1.0	17	1	US-08-373-124A-2149	Sequence 2149, Ap
263	12.4	1.0	15	1	US-08-313-492B-161	Sequence 160, App	C 336	12.2	1.0	17	1	US-08-373-124A-2151	Sequence 2151, Ap
264	12.4	1.0	15	1	US-08-313-492B-161	Sequence 161, App	C 337	12.2	1.0	17	1	US-08-373-124A-2157	Sequence 2157, Ap
265	12.4	1.0	15	1	US-08-085-658-52	Sequence 52, Appl	C 338	12.2	1.0	17	1	US-08-373-124A-2397	Sequence 2397, Ap
266	12.4	1.0	15	1	US-08-334-847-325	Sequence 325, App	C 339	12.2	1.0	17	1	US-08-435-628-742	Sequence 742, App
267	12.4	1.0	15	1	US-08-317-432A-4	Sequence 4, Appl	C 340	12.2	1.0	17	1	US-08-435-628-792	Sequence 792, App
268	12.4	1.0	15	1	US-08-311-486C-193	Sequence 193, App	C 341	12.2	1.0	17	1	US-08-435-628-792	Sequence 792, App
269	12.4	1.0	15	1	US-08-311-486C-202	Sequence 202, App	C 342	12.2	1.0	17	1	US-08-435-628-960	Sequence 960, App
270	12.4	1.0	15	1	US-08-311-486C-717	Sequence 717, App	C 343	12.2	1.0	17	1	US-08-435-628-962	Sequence 962, App
271	12.4	1.0	15	1	US-08-293-620A-217	Sequence 217, App	C 344	12.2	1.0	17	1	US-08-435-628-1048	Sequence 1048, Ap
272	12.4	1.0	15	1	US-08-293-620A-511	Sequence 511, App	C 345	12.2	1.0	17	1	US-08-435-628-1048	Sequence 1048, Ap
273	12.4	1.0	15	1	US-08-293-620A-751	Sequence 751, App	C 346	12.2	1.0	17	1	US-08-435-628-1058	Sequence 1058, Ap
274	12.4	1.0	15	1	US-08-604-871-3	Sequence 3, Appl	C 347	12.2	1.0	17	1	US-08-435-628-1871	Sequence 1871, Ap
275	12.4	1.0	15	1	US-08-604-871-4	Sequence 4, Appl	C 348	12.2	1.0	17	1	US-08-435-628-1885	Sequence 1885, Ap
276	12.4	1.0	15	1	US-08-585-684B-893	Sequence 893, App	C 349	12.2	1.0	17	1	US-08-435-628-1901	Sequence 1901, Ap
277	12.4	1.0	15	1	US-08-585-684B-2060	Sequence 2060, Ap	C 350	12.2	1.0	17	1	US-08-435-628-1983	Sequence 1983, Ap
278	12.4	1.0	15	1	US-08-471-907A-52	Sequence 52, Appl	C 351	12.2	1.0	17	1	US-08-435-628-2147	Sequence 2147, Ap
279	12.4	1.0	15	1	US-09-071-845-517	Sequence 217, App	C 352	12.2	1.0	17	1	US-08-435-628-2149	Sequence 2149, Ap
280	12.4	1.0	15	1	US-09-071-845-511	Sequence 511, App	C 353	12.2	1.0	17	1	US-08-435-628-2151	Sequence 2151, Ap
281	12.4	1.0	15	1	US-09-071-845-751	Sequence 751, App	C 354	12.2	1.0	17	1	US-08-435-628-2157	Sequence 2157, Ap
282	12.4	1.0	15	1	US-09-038-073-593	Sequence 893, App	C 355	12.2	1.0	17	1	US-08-435-628-2397	Sequence 2397, App
283	12.4	1.0	15	1	US-09-167-375-13	Sequence 2060, Ap	C 356	12.2	1.0	17	1	US-08-292-620A-1824	Sequence 1824, Ap
284	12.4	1.0	15	1	US-09-167-375-14	Sequence 13, Appl	C 357	12.2	1.0	17	1	US-08-292-620A-1845	Sequence 1845, Ap
285	12.4	1.0	15	1	US-09-167-375-14	Sequence 14, Appl	C 358	12.2	1.0	17	1	US-08-292-620A-1989	Sequence 1989, Ap
286	12.4	1.0	15	1	US-09-194-679-12	Sequence 12, Appl	C 359	12.2	1.0	17	1	US-08-292-620A-2007	Sequence 2007, Ap
287	12.4	1.0	15	1	US-08-584-040-8488	Sequence 8488, Ap	C 360	12.2	1.0	17	1	US-08-292-620A-2009	Sequence 2009, Ap
288	12.4	1.0	15	1	US-09-475-947A-180	Sequence 180, App	C 361	12.2	1.0	17	1	US-08-534-454-1	Sequence 1, Appl
289	12.4	1.0	15	1	US-09-371-772B-4142	Sequence 4142, Ap	C 362	12.2	1.0	17	1	US-08-467-963C-30	Sequence 30, Appl
290	12.4	1.0	15	1	US-08-962-690-21	Sequence 21, Appl	C 363	12.2	1.0	17	1	US-08-838-189D-30	Sequence 30, Appl
291	12.4	1.0	16	1	US-09-371-772B-5877	Sequence 5877, Ap	C 364	12.2	1.0	17	1	US-08-852-344D-30	Sequence 30, Appl
292	12.4	1.0	17	1	US-08-390-850-428	Sequence 428, App	C 365	12.2	1.0	17	1	US-08-344-639E-30	Sequence 30, Appl
293	12.4	1.0	17	1	US-08-373-124A-1437	Sequence 1437, Ap	C 366	12.2	1.0	17	1	US-08-855-058-1	Sequence 1, Appl
294	12.4	1.0	17	1	US-08-435-634-428	Sequence 428, App	C 367	12.2	1.0	17	1	US-08-985-162-365	Sequence 265, App
295	12.4	1.0	17	1	US-08-435-628-1437	Sequence 1437, Ap	C 368	12.2	1.0	17	1	US-08-985-162-775	Sequence 775, App
296	12.4	1.0	17	1	US-08-584-040-4227	Sequence 4227, Ap	C 369	12.2	1.0	17	1	US-08-923-558-4	Sequence 4, Appl
297	12.4	1.0	17	1	US-08-584-040-5646	Sequence 188, App	C 370	12.2	1.0	17	1	US-08-913-833-84	Sequence 84, Appl
298	12.4	1.0	17	1	US-08-584-040-1838	Sequence 1838, Ap	C 371	12.2	1.0	17	1	US-09-071-845-1824	Sequence 1824, Ap
299	12.4	1.0	17	1	US-08-584-040-2078	Sequence 2078, Ap	C 372	12.2	1.0	17	1	US-09-071-845-1845	Sequence 1845, Ap
300	12.4	1.0	17	1	US-08-584-040-2373	Sequence 2373, Ap	C 373	12.2	1.0	17	1	US-09-071-845-1989	Sequence 1989, Ap
301	12.4	1.0	17	1	US-08-584-040-2374	Sequence 2374, Ap	C 374	12.2	1.0	17	1	US-09-071-845-2007	Sequence 2007, Ap
302	12.4	1.0	17	1	US-08-584-040-3849	Sequence 3849, Ap	C 375	12.2	1.0	17	1	US-09-071-845-2009	Sequence 2009, Ap
303	12.4	1.0	17	1	US-08-584-040-4227	Sequence 4227, Ap	C 376	12.2	1.0	17	1	US-09-141-286-1	Sequence 1, Appl
304	12.4	1.0	17	1	US-08-584-040-5646	Sequence 5646, Ap	C 377	12.2	1.0	17	1	US-09-502-710-15	Sequence 15, Appl
305	12.4	1.0	17	1	US-08-584-040-7532	Sequence 7532, Ap	C 378	12.2	1.0	17	1	US-09-502-711-15	Sequence 15, Appl
306	12.4	1.0	17	1	US-08-584-040-7817	Sequence 7817, Ap	C 379	12.2	1.0	17	1	US-09-580-794C-84	Sequence 84, Appl
307	12.4	1.0	17	1	US-08-584-040-7819	Sequence 7819, Ap	C 380	12.2	1.0	17	1	US-08-584-040-1815	Sequence 1815, Ap
308	12.4	1.0	17	1	US-09-371-772B-383	Sequence 383, App	C 381	12.2	1.0	17	1	US-08-584-040-2050	Sequence 2050, Ap
309	12.4	1.0	17	1	US-09-371-772B-623	Sequence 623, App	C 382	12.2	1.0	17	1	US-08-584-040-2187	Sequence 2187, Ap
310	12.4	1.0	17	1	US-09-371-772B-918	Sequence 918, App	C 383	12.2	1.0	17	1	US-08-584-040-2304	Sequence 2304, Ap
311	12.4	1.0	17	1	US-09-371-772B-1616	Sequence 1616, Ap	C 384	12.2	1.0	17	1	US-08-584-040-2305	Sequence 2305, Ap
312	12.4	1.0	17	1	US-09-371-772B-1994	Sequence 1994, Ap	C 385	12.2	1.0	17	1	US-08-584-040-2339	Sequence 2339, Ap
313	12.4	1.0	17	1	US-09-371-772B-2536	Sequence 2536, Ap	C 386	12.2	1.0	17	1	US-08-584-040-2375	Sequence 2375, Ap
314	12.4	1.0	17	1	US-09-371-772B-3601	Sequence 3601, Ap	C 387	12.2	1.0	17	1	US-08-584-040-2555	Sequence 2555, Ap
315	12.4	1.0	17	1	US-09-371-772B-3603	Sequence 3603, Ap	C 388	12.2	1.0	17	1	US-08-584-040-3700	Sequence 2700, Ap
316	12.4	1.0	17	1	US-09-371-772B-4746	Sequence 4746, Ap	C 389	12.2	1.0	17	1	US-08-584-040-3701	Sequence 2701, Ap
317	12.4	1.0	17	1	US-09-371-772B-5229	Sequence 5229, Ap	C 390	12.2	1.0	17	1	US-08-584-040-3715	Sequence 2715, Ap
318	12.4	1.0	17	1	US-09-371-772B-5266	Sequence 5266, Ap	C 391	12.2	1.0	17	1	US-08-584-040-2794	Sequence 2794, Ap
319	12.4	1.0	17	1	US-09-371-772B-5290	Sequence 5290, Ap	C 392	12.2	1.0	17	1	US-08-584-040-2827	Sequence 2827, Ap
320	12.2	1.0	17	1	US-08-233-130A-10	Sequence 10, Appl	C 393	12.2	1.0	17	1	US-08-584-040-2857	Sequence 2857, Ap
321	12.2	1.0	17	1	US-08-233-130A-11	Sequence 11, Appl	C 394	12.2	1.0	17	1	US-08-584-040-3848	Sequence 3848, Ap
322	12.2	1.0	17	1	US-08-373-124A-742	Sequence 742, App	C 395	12.2	1.0	17	1	US-08-584-040-3986	Sequence 3986, Ap
323	12.2	1.0	17	1	US-08-373-124A-792	Sequence 792, App	C 396	12.2	1.0	17	1	US-08-584-040-4259	Sequence 4259, Ap
324	12.2	1.0	17	1	US-08-373-124A-792	Sequence 792, App	C 397	12.2	1.0	17	1	US-08-584-040-7945	Sequence 7945, Ap
325	12.2	1.0	17	1	US-08-373-124A-960	Sequence 960, App	C 398	12.2	1.0	17	1	US-08-584-040-7962	Sequence 7962, Ap

545	11.6	0.9	19	1	US-09-626-929-23	Sequence 23, Appl	618	11.4	0.9	15	1	US-08-311-486C-701	Sequence 701, App
546	11.6	0.9	19	1	US-09-484-850-23	Sequence 23, Appl	619	11.4	0.9	15	1	US-08-311-486C-722	Sequence 722, App
547	11.6	0.9	19	1	US-09-408-332-23	Sequence 23, Appl	C 620	11.4	0.9	15	1	US-08-292-620A-149	Sequence 149, App
548	11.6	0.9	19	1	US-09-626-930-23	Sequence 23, Appl	621	11.4	0.9	15	1	US-08-292-620A-218	Sequence 218, App
549	11.6	0.9	19	1	US-09-626-528-23	Sequence 23, Appl	622	11.4	0.9	15	1	US-08-292-620A-512	Sequence 512, App
550	11.6	0.9	19	1	US-09-626-585-23	Sequence 23, Appl	623	11.4	0.9	15	1	US-08-292-620A-513	Sequence 513, App
551	11.6	0.9	19	1	US-09-694-883-23	Sequence 23, Appl	624	11.4	0.9	15	1	US-08-292-620A-516	Sequence 516, App
552	11.6	0.9	19	1	US-08-487-759-1	Sequence 1, Appl	625	11.4	0.9	15	1	US-08-292-620A-518	Sequence 518, App
553	11.6	0.9	19	1	US-08-807-104-1	Sequence 1, Appl	626	11.4	0.9	15	1	US-08-292-620A-576	Sequence 576, App
554	11.6	0.9	19	1	US-08-807-104-4	Sequence 4, Appl	C 627	11.4	0.9	15	1	US-08-585-684B-894	Sequence 894, App
555	11.6	0.9	19	1	US-08-807-104-6	Sequence 6, Appl	C 628	11.4	0.9	15	1	US-08-716-308-14	Sequence 14, Appl
556	11.6	0.9	19	1	US-08-807-104-7	Sequence 7, Appl	C 629	11.4	0.9	15	1	US-08-466-860-58	Sequence 58, Appl
557	11.6	0.9	19	1	US-08-807-104-8	Sequence 8, Appl	C 630	11.4	0.9	15	1	US-08-544-381B-104	Sequence 104, Appl
558	11.6	0.9	19	1	US-08-807-104-9	Sequence 9, Appl	631	11.4	0.9	15	1	US-08-913-833-30	Sequence 30, Appl
559	11.6	0.9	19	1	US-08-807-104-10	Sequence 10, Appl	632	11.4	0.9	15	1	US-08-913-833-148	Sequence 148, Appl
560	11.6	0.9	19	1	US-08-807-104-13	Sequence 13, Appl	C 633	11.4	0.9	15	1	US-08-472-040A-58	Sequence 58, Appl
561	11.6	0.9	19	1	US-08-807-104-14	Sequence 14, Appl	634	11.4	0.9	15	1	US-09-071-845-149	Sequence 149, App
562	11.6	0.9	19	1	US-08-807-104-15	Sequence 15, Appl	C 635	11.4	0.9	15	1	US-09-071-845-218	Sequence 218, App
563	11.6	0.9	19	1	US-08-807-104-16	Sequence 16, Appl	636	11.4	0.9	15	1	US-09-071-845-512	Sequence 512, App
564	11.6	0.9	19	1	US-08-973-137-1	Sequence 1, Appl	637	11.4	0.9	15	1	US-09-071-845-513	Sequence 513, App
565	11.6	0.9	19	1	US-08-480-068-1	Sequence 1, Appl	638	11.4	0.9	15	1	US-09-071-845-516	Sequence 516, App
566	11.6	0.9	19	1	US-08-480-068-4	Sequence 4, Appl	639	11.4	0.9	15	1	US-09-071-845-518	Sequence 518, App
567	11.6	0.9	19	1	US-08-480-068-6	Sequence 6, Appl	640	11.4	0.9	15	1	US-09-071-845-518	Sequence 518, App
568	11.6	0.9	19	1	US-08-480-068-7	Sequence 7, Appl	641	11.4	0.9	15	1	US-08-952-376-3	Sequence 3, Appl
569	11.6	0.9	19	1	US-08-480-068-8	Sequence 8, Appl	C 642	11.4	0.9	15	1	US-09-038-073-894	Sequence 894, App
570	11.6	0.9	19	1	US-08-480-068-9	Sequence 9, Appl	C 643	11.4	0.9	15	1	US-08-276-776-58	Sequence 58, Appl
571	11.6	0.9	19	1	US-08-480-068-10	Sequence 10, Appl	C 644	11.4	0.9	15	1	US-08-471-209-58	Sequence 58, Appl
572	11.6	0.9	19	1	US-08-480-068-13	Sequence 13, Appl	645	11.4	0.9	15	1	US-09-253-977-4	Sequence 4, Appl
573	11.6	0.9	19	1	US-08-480-068-14	Sequence 14, Appl	646	11.4	0.9	15	1	US-09-580-794C-30	Sequence 30, Appl
574	11.6	0.9	19	1	US-08-480-068-15	Sequence 15, Appl	647	11.4	0.9	15	1	US-09-580-794C-148	Sequence 148, App
575	11.6	0.9	19	1	US-08-480-068-16	Sequence 16, Appl	C 648	11.4	0.9	15	1	US-09-081-646-236	Sequence 236, App
576	11.6	0.9	19	1	US-08-973-137-1	Sequence 1, Appl	649	11.4	0.9	15	1	US-09-081-646-575	Sequence 575, App
577	11.6	0.9	19	1	US-08-973-137-4	Sequence 4, Appl	C 650	11.4	0.9	15	1	US-09-423-233-40	Sequence 40, Appl
578	11.6	0.9	19	1	US-08-973-137-6	Sequence 6, Appl	651	11.4	0.9	15	1	US-09-445-301A-36	Sequence 36, Appl
579	11.6	0.9	19	1	US-08-973-137-7	Sequence 7, Appl	652	11.4	0.9	15	1	US-09-099-932-40	Sequence 40, Appl
580	11.6	0.9	19	1	US-08-973-137-8	Sequence 8, Appl	C 653	11.4	0.9	16	1	US-08-281-106-46	Sequence 46, Appl
581	11.6	0.9	19	1	US-08-973-137-9	Sequence 9, Appl	C 654	11.4	0.9	16	1	US-08-403-634-27	Sequence 27, Appl
582	11.6	0.9	19	1	US-08-973-137-10	Sequence 10, Appl	C 655	11.4	0.9	16	1	US-08-551-275-6	Sequence 6, Appl
583	11.6	0.9	19	1	US-08-973-137-13	Sequence 13, Appl	C 656	11.4	0.9	16	1	US-08-501-968-36	Sequence 36, Appl
584	11.6	0.9	19	1	US-08-973-137-14	Sequence 14, Appl	C 657	11.4	0.9	16	1	US-08-485-942A-87	Sequence 87, Appl
585	11.6	0.9	19	1	US-08-973-137-15	Sequence 15, Appl	658	11.4	0.9	16	1	US-08-913-833-149	Sequence 149, App
586	11.6	0.9	19	1	US-08-973-137-16	Sequence 16, Appl	659	11.4	0.9	16	1	US-08-488-214A-87	Sequence 87, Appl
587	11.6	0.9	19	1	PCT-US96-08320-1	Sequence 1, Appl	660	11.4	0.9	16	1	US-08-488-208A-87	Sequence 87, Appl
588	11.6	0.9	19	1	PCT-US96-08330-1	Sequence 1, Appl	C 661	11.4	0.9	16	1	US-08-913-441B-2	Sequence 2, Appl
589	11.6	0.9	20	1	US-09-433-694-61	Sequence 61, Appl	662	11.4	0.9	16	1	US-08-483-211A-87	Sequence 87, Appl
590	11.6	0.9	20	1	US-09-658-687A-26	Sequence 26, Appl	C 663	11.4	0.9	16	1	US-09-303-029A-2	Sequence 2, Appl
591	11.6	0.9	20	1	US-08-807-104-2	Sequence 2, Appl	C 664	11.4	0.9	16	1	US-09-580-794C-149	Sequence 149, App
592	11.6	0.9	20	1	US-08-480-068-2	Sequence 2, Appl	665	11.4	0.9	16	1	US-08-488-223A-87	Sequence 87, Appl
593	11.6	0.9	20	1	US-08-973-137-2	Sequence 2, Appl	C 667	11.4	0.9	16	1	US-08-533-243-17	Sequence 17, Appl
594	11.4	0.9	13	1	US-08-233-130A-1	Sequence 1, Appl	C 668	11.4	0.9	16	1	US-08-488-225A-87	Sequence 87, Appl
595	11.4	0.9	13	1	US-08-496-631-4	Sequence 4, Appl	C 669	11.4	0.9	16	1	US-09-199-269-46	Sequence 46, Appl
596	11.4	0.9	13	1	US-08-441-887A-124	Sequence 124, App	C 670	11.4	0.9	16	1	US-09-602-586-2	Sequence 2, Appl
597	11.4	0.9	13	1	US-09-183-846A-12	Sequence 12, Appl	C 671	11.4	0.9	16	1	US-09-371-772B-5689	Sequence 5689, App
598	11.4	0.9	13	1	US-08-961-578C-12	Sequence 12, Appl	C 672	11.4	0.9	16	1	US-09-371-772B-5928	Sequence 5928, App
599	11.4	0.9	13	1	US-08-551-275-7	Sequence 7, Appl	C 673	11.4	0.9	16	1	US-09-371-772B-5976	Sequence 5976, App
600	11.4	0.9	14	1	US-08-715-568A-7	Sequence 7, Appl	C 674	11.4	0.9	16	1	PCT-US96-10984-36	Sequence 36, Appl
601	11.4	0.9	14	1	US-08-913-833-146	Sequence 146, App	C 675	11.4	0.9	16	1	US-08-584-040-2785	Sequence 2785, App
602	11.4	0.9	14	1	US-08-872-917-6	Sequence 6, Appl	C 676	11.4	0.9	17	1	US-09-371-772B-1309	Sequence 1309, App
603	11.4	0.9	14	1	US-09-194-679-11	Sequence 11, Appl	C 677	11.4	0.9	17	1	US-09-371-772B-5584	Sequence 5584, App
604	11.4	0.9	14	1	US-09-580-794C-146	Sequence 146, App	C 678	11.4	0.9	17	1	US-09-371-772B-5962	Sequence 7962, App
605	11.4	0.9	14	1	US-08-535-249-110	Sequence 110, App	C 679	11.4	0.9	17	1	US-08-584-040-7962	Sequence 3745, App
606	11.4	0.9	14	1	US-09-473-947A-148	Sequence 148, App	C 680	11.4	0.9	20	1	US-09-371-772B-3745	Sequence 83, Appl
607	11.4	0.9	14	1	US-09-473-947A-310	Sequence 310, App	C 681	11.4	0.9	16	1	US-08-488-744A-83	Sequence 7, Appl
608	11.4	0.9	15	1	US-08-473-248-10	Sequence 10, Appl	C 682	11.2	0.9	16	1	US-08-243-402-7	Sequence 22, Appl
609	11.4	0.9	15	1	US-08-313-492B-114	Sequence 114, App	C 683	11.2	0.9	16	1	US-08-683-423-22	Sequence 22, Appl
610	11.4	0.9	15	1	US-08-313-492B-115	Sequence 115, App	C 684	11.2	0.9	16	1	PCT-US95-05141-22	Sequence 9, Appl
611	11.4	0.9	15	1	US-08-313-492B-122	Sequence 122, App	C 685	11.2	0.9	17	1	US-08-146-421-9	Sequence 1838, App
612	11.4	0.9	15	1	US-08-334-847-42	Sequence 42, Appl	C 686	11.2	0.9	17	1	US-08-584-040-1838	Sequence 1838, App
613	11.4	0.9	15	1	US-08-334-847-43	Sequence 43, Appl	C 687	11.2	0.9	17	1	US-08-584-040-7532	Sequence 7532, App
614	11.4	0.9	15	1	US-08-440-787A-117	Sequence 117, App	C 688	11.2	0.9	17	1	US-08-371-772B-383	Sequence 383, App
615	11.4	0.9	15	1	US-08-671-071B-4	Sequence 4, Appl	C 689	11.2	0.9	17	1	US-08-373-124A-960	Sequence 960, App
616	11.4	0.9	15	1	US-08-311-486C-203	Sequence 203, App	C 690	11.2	0.9	17	1	US-08-373-124A-2149	Sequence 2149, App
617	11.4	0.9	15	1	US-08-311-486C-700	Sequence 700, App							

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

S-08-246-855A-16

Query Match 1.7%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 403 TCTGTGATCCAGATCAG 423

b 21 TCTGTGATCCAGATCAG 1

RESULT 4

CT-US95-06356-16/c

Sequence 16, Application PC/TUS9506356

GENERAL INFORMATION:

APPLICANT: NAME: BOARD OF REGENTS, THE UNIVERSITY OF TEXAS
APPLICANT: SYSTEM
APPLICANT: STREET: 201 West 7th Street
APPLICANT: CITY: Austin
APPLICANT: STATE: Texas
APPLICANT: COUNTRY: United States of America
APPLICANT: POSTAL CODE: 78701
APPLICANT: TELEPHONE NO: (512)499-4462
APPLICANT: TELEFAX: (512)499-4523
TITLE OF INVENTION: COMPOSITIONS AND USES THEREOF
TITLE OF INVENTION: IN THE DIAGNOSIS OF PSORIASIS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD449P--
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06356
FILING DATE: CONCURRENTLY HERewith

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,855
FILING DATE: 20 MAY 1994

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

TT-US95-06356-16

Query Match

Best Local Similarity 1.7%; Score 21; DB 1; Length 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 TCTGTGATCCAGATCAG 423

Db 21 TCTGTGATCCAGATCAG 1

RESULT 5

US-09-046-894-11/c

Sequence 11, Application US/09046894

Patent No. 6190857

GENERAL INFORMATION:

APPLICANT: Ralph, David
APPLICANT: An, Gang
APPLICANT: O'Hara, Mark S.
APPLICANT: Veltre, Robert
TITLE OF INVENTION: DIAGNOSIS OF DISEASE STATE USING mRNA
TITLE OF INVENTION: PROFILES IN PERIPHERAL LEUKOCYTES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,894
FILING DATE: Concurrently Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,576
FILING DATE: 24-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:014

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-046-894-11

Query Match 1.6%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 GGTCTGTTGATGAGTTGCCA 499

Db 20 GGTCTGTTGATGAGTTGCCA 1

RESULT 6

US-09-165-868-8

Sequence 8, Application US/09165868

Patent No. 6465176

GENERAL INFORMATION:

APPLICANT: Message Pharmaceuticals, Inc.
TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPOUNDS
TITLE OF INVENTION: AFFECTING RNA/RNA BINDING PROTEIN INTERACTIONS
FILE REFERENCE: 50093/003W01
CURRENT APPLICATION NUMBER: US/09/165,868
CURRENT FILING DATE: 1998-10-02

;; PRIOR APPLICATION NUMBER: PCT/US99/21672
;; PRIOR FILING DATE: 1999-09-16
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 8
;; LENGTH: 21
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-09-165-868-8

Query Match 1.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 26.3%; Pred. No. 24;
Matches 5; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 1044 TATTATGATTTATTTA 1062
DB 3 UUAUUUAUUUAUUUA 21

RESULT 7
US-09-433-694-61/c
; Sequence 61, Application US/09433694
; Patent No. 6165790
; GENERAL INFORMATION:
; APPLICANT: Alexander H. Borchers
; APPLICANT: Donna T. Ward
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF P13 KINASE P55 GAMMA EXPRESSION
; FILE REFERENCE: RTS-0098
; CURRENT APPLICATION NUMBER: US/09/433,694
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-433-694-61

Query Match 1.3%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1606 ATGAACATTTAAATAT 1623
DB 20 ATGAACATTTAAATAT 3

RESULT 8
US-08-619-542B-58/c
; Sequence 58, Application US/08619542B
; Patent No. 5830662
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in the City
; APPLICANT: of New York
; TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
; TITLE OF INVENTION: CDNA LIBRARIES
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/619,542B
;; FILING DATE: June 21, 1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 42840-A-PCT-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 278-0400
;; TELEFAX: (212) 391-0525
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 58:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 22 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ANTI-SENSE: YES
US-08-619-542B-58

Query Match 1.3%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1068 CAATATTTGTGCAAGATTT 1088
DB 21 CAATATTTGCCAGATTT 1

RESULT 9
US-09-422-978-7355
; Sequence 7355, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7355
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-3893 for SEQ 3421,
US-09-422-978-7355

Query Match 1.3%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 901 CTGGTTTCCTTTATTT 919
DB 1 CTGGTTTCCTTTATTT 19

RESULT 10
US-08-123-449A-1/c
; Sequence 1, Application US/08123449A
; Patent No. 5583032

```

GENERAL INFORMATION:
APPLICANT: TORRENCE, PAUL
APPLICANT: ROBERT, SILVERMAN
APPLICANT: RATAN, MAITRA
APPLICANT: KRISTYNA, LESIAK
TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS version
SOFTWARE: FastSeq Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,449A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10103
FILING DATE: 10-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH034.001QPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-123-449A-1

Query Match 1.2%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

/ 616 ACACAAACACACAAATATTTT 637
3 22 AAAAAAAAAAAAAAAAAATTTT 1

RESULT 11
3-08-123-449A-2/c
Sequence 2, Application US/08123449A
Patent No. 5583032
GENERAL INFORMATION:
APPLICANT: TORRENCE, PAUL
APPLICANT: ROBERT, SILVERMAN
APPLICANT: RATAN, MAITRA
APPLICANT: KRISTYNA, LESIAK
TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: CA
COUNTRY: USA

```

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ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS version
SOFTWARE: FastSeq Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,449A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10103
FILING DATE: 10-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH034.001QPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-123-449A-2

Query Match 1.2%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 616 ACACAAACACACAAATATTTT 637
DB 22 AAAAAAAAAAAAAAAAAATTTT 1

RESULT 12
US-08-458-050-1/c
Sequence 1, Application US/08458050
Patent No. 5677289
GENERAL INFORMATION:
APPLICANT: TORRENCE, PAUL
APPLICANT: ROBERT, SILVERMAN
APPLICANT: RATAN, MAITRA
APPLICANT: KRISTYNA, LESIAK
TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS version
SOFTWARE: FastSeq Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,050
FILING DATE: 01-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,449
FILING DATE: 17-SEP-1993
APPLICATION NUMBER: PCT/US93/10103

```

FILING DATE: 10-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH034.001QPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLECULE TYPE: cdna

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

US-08-458-050-1

Query Match 1.2%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 616 ACAAACACACAAATAATTTT 637
DB 22 AAAAAAAAAAAAAAAAAATTTT 1

RESULT 13

US-08-458-050-2/c

Sequence 2, Application US/08458050

Patent No. 5677289

GENERAL INFORMATION:

APPLICANT: TORRENCE, PAUL

APPLICANT: ROBERT, SILVERMAN

APPLICANT: RATAN, MAITRA

APPLICANT: KRISTINA, LESIAK

TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES

TITLE OF INVENTION: OF RNA

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson and Bear

STREET: 620 Newport Center Drive

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS version

SOFTWARE: FastSeq Version 1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458,050

FILING DATE: 01-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/123,449

FILING DATE: 17-SEP-1993

APPLICATION NUMBER: PCT/US93/10103

FILING DATE: 10-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Fedrick, Michael F.

REGISTRATION NUMBER: 36,799

REFERENCE/DOCKET NUMBER: NIH034.001QPC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 714-760-0404

TELEFAX: 714-760-9502

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-458-050-2

Query Match 1.2%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 616 ACAAACACACAAATAATTTT 637
DB 22 AAAAAAAAAAAAAAAAAATTTT 1

RESULT 14

US-08-950-196-1/c

Sequence 1, Application US/08950196

Patent No. 6271369

GENERAL INFORMATION:

APPLICANT: TORRENCE, PAUL

APPLICANT: ROBERT, SILVERMAN

APPLICANT: RATAN, MAITRA

APPLICANT: KRISTINA, LESIAK

TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES

TITLE OF INVENTION: OF RNA

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson and Bear

STREET: 620 Newport Center Drive

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS version

SOFTWARE: FastSeq Version 1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/950,196

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/123,449

FILING DATE:

APPLICATION NUMBER: PCT/US93/10103

FILING DATE: 10-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Fedrick, Michael F.

REGISTRATION NUMBER: 36,799

REFERENCE/DOCKET NUMBER: NIH034.001QPC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 714-760-0404

TELEFAX: 714-760-9502

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

US-08-950-196-1

Query Match 1.2%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 85;

Matches 18; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

Y 616 ACAAAACAAACAAATATTT 637
b 22 AAAAAAAAAAAAAAAAAATTT 1

RESULT 15

S-08-950-196-2/c
Sequence 2, Application US/08950196
Patent No. 6271369

GENERAL INFORMATION:

APPLICANT: TORRENCE, PAUL
APPLICANT: ROBERT, SILVERMAN
APPLICANT: RATAN, MAITRA
APPLICANT: KRISTINA, LESIAK
TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
TITLE OF INVENTION: OF RNA
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS version
SOFTWARE: FastSeq Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,196
FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/123,449
FILING DATE:

APPLICATION NUMBER: PCT/US93/10103

FILING DATE: 10-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Pedrick, Michael P.

REGISTRATION NUMBER: 36,799

REFERENCE/DOCKET NUMBER: NIH034.001QPC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 714-760-0404

TELEFAX: 714-760-9502

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHEICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

S-08-950-196-2

Query Match 1.2%; Score 15.6; DB 1; Length 22;

Best Local Similarity 81.8%; Pred. No. 85;

Matches 18; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

Y 616 ACAAAACAAACAAATATTT 637
b 22 AAAAAAAAAAAAAAAAAATTT 1

RESULT 16

S-08-146-421-9

Sequence 9, Application US/08146421
Patent No. 5543499

GENERAL INFORMATION:

APPLICANT: BREWER, GARY
TITLE OF INVENTION: DNA SEQUENCE ENCODING A POLYPEPTIDE WITH
TITLE OF INVENTION: ANTI-TUMOR PROPERTIES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: DILWORTH & BARRESE
STREET: 4350 LA JOLLA VILLAGE DRIVE, SUITE 300
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,421
FILING DATE: 29-OCT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 489-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4410
TELEFAX: 619-453-2839
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
US-08-146-421-9

Query Match 1.2%; Score 15.4; DB 1; Length 17;

Best Local Similarity 29.4%; Pred. No. 46;

Matches 5; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

Y 1046 ATTATGATTTATTTA 1062

Db 1 AUUUAUUUAUUUUUA 17

RESULT 17

US-09-205-144-43

Sequence 43, Application US/09205144

Patent No. 5958771

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Elizabeth J. Ackermann

APPLICANT: Lex M. Cowsett

TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2 EXPRESS

FILE REFERENCE: RTS-0021

CURRENT APPLICATION NUMBER: US/09/205,144

CURRENT FILING DATE: 1998-12-03

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 43

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-205-144-43

Query Match 1.2%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 54;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1294 CTGAAATTTTATTTGAA 1310

Db 1 CTGAAATTTTATTTGAA 17


```
RESULT 18
IS-09-488-744A-83/c
Sequence 83, Application US/09488744A
Patent No. 6287860
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: William Gaarde
APPLICANT: Donna T. Ward
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF MEK2 EXPRESSION
FILE REFERENCE: RTS-0108
CURRENT APPLICATION NUMBER: US/09/488,744A
CURRENT FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 83
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
IS-09-488-744A-83
Query Match 1.2%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 512 GATTCCTGGTTAAATTT 528
|||||
DB 17 GATTCCTGGTTAAATTT 1

RESULT 19
IS-08-943-731-521
Sequence 521, Application US/08943731
Patent No. 6265157
GENERAL INFORMATION:
APPLICANT: PROCKOP, DARWIN J.
APPLICANT: SPOTILA, LORETTA D.
APPLICANT: DELTAS, CONSTANTINOS D.
APPLICANT: SEREDA, LARISA
APPLICANT: LARSON, ANDREA W.
APPLICANT: PACK, MICHAEL
APPLICANT: COLIGE, ALAIN
APPLICANT: EARLY, JAMES
APPLICANT: KORKKO, JARMO
APPLICANT: ALA-KORKKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLR.
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 521:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-943-731-521
Query Match 1.2%; Score 15.4; DB 1; Length 22;
Best Local Similarity 94.1%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 421 CAGTGAAGATGCCAGTG 437
|||||
DB 1 CAGTGAAGATGCCAGAG 17

RESULT 20
US-07-922-723A-29/c
Sequence 29, Application US/07922723A
Patent No. 5369004
GENERAL INFORMATION:
APPLICANT: Drs. Mihal H. Polymeropoulos
APPLICANT: and Carl R. Merrill
TITLE OF INVENTION: FIVE HIGHLY INFORMATIVE
TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe Price, LeBlanc & Becker
STREET: Suite 300, 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/922,723A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: D.J. Mills
REGISTRATION NUMBER: 34506
REFERENCE/DOCKET NUMBER: 717081B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-922-723A-29
Query Match 1.2%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 427 AGATGCCAGTGAACCTTCAA 446
Db 20 ACATGCCAGTGACACTTCCA 1

RESULT 21
US-07-799-828C-29/c
; Sequence 29, Application US/07799828C
; Patent No. 5378502
; GENERAL INFORMATION:
; APPLICANT: Drs. Carl R. Merrill and
; APPLICANT: Michael H. Polymeropoulos
; TITLE OF INVENTION: TWENTY SEVEN HIGHLY INFORMATIVE
; MICROSTELLITE REPEAT
; TITLE OF INVENTION: POLYMORPHIC DNA MARKERS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/799,828C
; FILING DATE: 19911127
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: D.J. Mills
; REGISTRATION NUMBER: 34,506
; REFERENCE/DOCKET NUMBER: 717081A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-799-828C-29

Query Match 1.2%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 427 AGATGCCAGTGAACCTTCAA 446
Db 20 ACATGCCAGTGACACTTCCA 1

RESULT 22
US-07-799-828C-29/c
; Sequence 29, Application US/07952277A
; Patent No. 5861504
; GENERAL INFORMATION:
; APPLICANT: Drs. Michael H. Polymeropoulos
; APPLICANT: and Carl R. Merrill
; TITLE OF INVENTION: ELEVEN HIGHLY INFORMATIVE
; MICROSTELLITE REPEAT POLYMORPHIC DNA MARKERS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314

Query Match 1.2%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 427 AGATGCCAGTGAACCTTCAA 446
Db 20 ACATGCCAGTGACACTTCCA 1

RESULT 23
US-09-780-173A-92/c
; Sequence 92, Application US/09780173A
; Patent No. 6455307
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA PRIME EXPRESSION
; FILE REFERENCE: RTS-0165
; CURRENT APPLICATION NUMBER: US/09/780,173A
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 92
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-780-173A-92

Query Match 1.2%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 633 ATTCTTGAATATAGGATTT 652
Db 20 ATTATTGAATATAAGGTTT 1

RESULT 24
US-08-377-687-53/c
; Sequence 53, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERBAS, FRANKY R.G.
```

```

;
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
;
; PRIOR APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-377-687-53
;
; Query Match 1.2%; Score 15.2; DB 1; Length 21;
; Best Local Similarity 85.0%; Pred. No. 96;
; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
Qy 688 AAATTGGCCCAAGGGCCAAG 707
Db 20 AAGTTGTGCCAAGGCCAAG 1
;
; RESULT 25
; US-08-377-192-53/c
; Sequence 53, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE: 17-JAN-1993
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
;

```

```

;
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-777-192-53
;
; Query Match 1.2%; Score 15.2; DB 1; Length 21;
; Best Local Similarity 85.0%; Pred. No. 96;
; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
Qy 688 AAATTGGCCCAAGGGCCAAG 707
Db 20 AAGTTGTGCCAAGGCCAAG 1
;
; RESULT 26
; US-08-971-982-53/c
; Sequence 53, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,982
; FILING DATE: 17-JAN-1997
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
;

```

```

; FILING DATE: March 26, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Licata, Jane Massey
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-810-1515
; TELEFAX: 609-810-1454
; INFORMATION FOR SEQ ID NO: 239:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-09-280-805-239
;
; Query Match 1.2%; Score 14.8; DB 1; Length 20;
; Best Local Similarity 88.9%; Pred. No. 1.1e+02;
; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 1017 TTCAGTGTAACTATTATTA 1034
DB 18 TTAAAGTAACTATTATTA 1
;
RESULT 29
US-09-496-694B-239
; Sequence 239, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 239
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-496-694B-239
;
; Query Match 1.2%; Score 14.8; DB 1; Length 20;
; Best Local Similarity 88.9%; Pred. No. 1.1e+02;
; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 1039 ATTTATTATTATCTATT 1056
DB 2 AGTTATTATTTTTGATT 19
;
RESULT 30
US-09-496-694B-240
; Sequence 240, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B

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; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 249
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; JS-09-496-694B-240

Query Match 1.2% Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2Y 1039 ATTATTATTATTGTAATT 1056
| | | | | | | | | | | | | | | | | | | | | |
Db 3 AGTTATTATTGTTGTAATT 20

RESULT 31
US-09-658-687A-26/c
; Sequence 26, Application US/09658687A
; Patent No. 6387699
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF A20 EXPRESSION
; FILE REFERENCE: RTS-0141
; CURRENT APPLICATION NUMBER: US/09/658,687A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-658-687A-26

Query Match 1.2% Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1237 ATTTCATTTCAGATAAA 1254
| | | | | | | | | | | | | | | | | | | | | |
Db 18 ATTGTCATTTCAGACAAA 1

RESULT 32
US-08-261-825-7/c
; Sequence 7, Application US/08261825
; Patent No. 5558993
; GENERAL INFORMATION:
; APPLICANT: Champion, Cheryl I.
; APPLICANT: Lovett, Michael A.
; APPLICANT: Haake, David A.
; APPLICANT: Miller, James N.
; APPLICANT: Blanco, David R.
; TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,825
; FILING DATE: 17-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN, LISA A.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: PD3516
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: OspA-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..21
; US-08-261-825-7

Query Match 1.2% Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 542 CAATCAATAGTTTTCAT 559
| | | | | | | | | | | | | | | | | | | | | |
Db 18 CAATAAATATTTTTCAT 1

RESULT 33
US-08-719-124-7/c
; Sequence 7, Application US/08719124
; Patent No. 5854395
; GENERAL INFORMATION:
; APPLICANT: Champion, Cheryl I.
; APPLICANT: Lovett, Michael A.
; APPLICANT: Haake, David A.
; APPLICANT: Miller, James N.
; APPLICANT: Blanco, David R.
; TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/719,124
; FILING DATE: 24-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/261,825
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN, LISA A.
; REGISTRATION NUMBER: P-38,347

REFERENCE/DOCKET NUMBER: PD3516
 TELEPHONE: (619) 455-5100
 TELEFAX: (619) 455-5110
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 IMMEDIATE SOURCE:
 CLONE: OspA-1
 NAME/KEY: CDS
 LOCATION: 1..21
 3-08-719-124-7

Query Match 1.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 542 CAATGAATAGTTTTCAT 559
 |||||
 18 CAATAAATATTTTCAT 1

RESULT 34
 3-09-461-697-307
 Sequence 307, Application US/09461697
 Patent No. 6277974
 GENERAL INFORMATION:
 APPLICANT: COGENT NEUROSCIENCE, Inc.
 APPLICANT: Lo, Donald C.
 APPLICANT: Barney, Shawn
 APPLICANT: Thomas, Mary Beth
 APPLICANT: Portbury, Stuart D.
 APPLICANT: Puranam, Kasturi
 APPLICANT: Katz, Lawrence C.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
 TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
 FILE REFERENCE: 10001-005-999
 CURRENT APPLICATION NUMBER: US/09/461,697
 NUMBER OF SEQ ID NOS: 466
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 307
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Homo sapiens
 3-09-461-697-307

Query Match 1.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 830 GGATTTTTCGTGTTAA 847
 |||||
 4 GGATTTTTCGTGTTAA 21

RESULT 35
 3-09-422-978-10751/c
 Sequence 10751, Application US/09422978
 Patent No. 6537751
 GENERAL INFORMATION:
 APPLICANT: Cohen, Daniel
 APPLICANT: Blumenfeld, Marta
 APPLICANT: Chumakov, Ilya
 TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
 FILE REFERENCE: GENSET.020CPI
 CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT FILING DATE: 1999-10-20
 EARLIER APPLICATION NUMBER: US 09/298,850
 EARLIER FILING DATE: 1999-04-21
 EARLIER APPLICATION NUMBER: US 60/109,732
 EARLIER FILING DATE: 1998-11-23
 EARLIER APPLICATION NUMBER: US 60/082,614
 EARLIER FILING DATE: 1998-04-21
 NUMBER OF SEQ ID NOS: 11796
 SEQ ID NO 10751
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Homo Sapiens
 FEATURE:
 NAME/KEY: primer_bind
 LOCATION: 1..21
 OTHER INFORMATION: downstream amplification primer 99-19601 for SEQ 2886, in complen
 US-09-422-978-10751

Query Match 1.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1593 TATAAAGTAAATATGAA 1610
 |||||
 20 TATAAAGGAAAGATGAA 3

RESULT 36
 PCT-US95-07748-7/c
 Sequence 7, Application PC/TUS9507748
 GENERAL INFORMATION:
 APPLICANT: The Regents of the University of California
 TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE
 TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: California
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/07748
 FILING DATE: 16-JUN-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: HAILE, LISA A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07419/013W01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 678-5070
 TELEFAX: (619) 678-5099
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 IMMEDIATE SOURCE:
 CLONE: OspA-1
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..21
 PCT-US95-07748-7

Query Match 1.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 542 CAATGAATAGTTTTCAT 559
|||||
Db 18 CAATAAATATTTTTCAT 1

RESULT 37
PCT-US95-07748A-7/c
; Sequence 7, Application PC/TUS9507748A
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07748A
; FILING DATE: 16-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILE, Ph.D., LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07419/013W01 (PD3516)
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: Ospa-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..21
PCT-US95-07748A-7

Query Match 1.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 542 CAATGAATAGTTTTCAT 559
|||||
Db 18 CAATAAATATTTTTCAT 1

RESULT 38
US-09-371-772B-4900
; Sequence 4900, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4900
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4900

Query Match 1.2%; Score 14.4; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 86;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 441 CTTCAAGCAATCTTAC 456
|:|||||:|
Db 1 CUCAAGCAAAUGUAC 16

RESULT 39
US-09-626-929-23
; Sequence 23, Application US/09626929
; Patent No. 6319714
; GENERAL INFORMATION:
; APPLICANT: CRAMERI, ANDREAS
; APPLICANT: STEMMER, WILHEM P.C.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: BASS, STEVEN H.
; APPLICANT: WELCH, MARK
; APPLICANT: NESS, JON E.
; APPLICANT: GUSTAFSSON, CLAES
; APPLICANT: PATTEN, PHILIP A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
; FILE REFERENCE: 02-029620US
; CURRENT APPLICATION NUMBER: US/09/626,929
; 2000-07-27
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/408,392
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/118,813
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/141,049
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-626-929-23

Query Match 1.1%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1102 ATGAATCATTTGATTA 1120
|||||
Db 1 ATGAATAATGTTTGAATA 19

RESULT 40
US-09-484-850-23
; Sequence 23, Application US/09484850
; Patent No. 6368861
; GENERAL INFORMATION:

APPLICANT: CRAMERI, ANDREAS
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: MINSHULL, JEREMY
APPLICANT: BASS, STEVEN H.
APPLICANT: WELCH, MARK
APPLICANT: NESS, JON E.
APPLICANT: GUSTAFSSON, CLAES
APPLICANT: PATTEN, PHILLIP A.
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
FILE REFERENCE: 02-029620US
CURRENT APPLICATION NUMBER: US/09/484,850
CURRENT FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: 09/408,392
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 60/118,813
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 60/141,049
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
3'-09-484-850-23
Query Match 1.1%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1102 ATGAATCATTGATTGAATA 1120
|||||
1 ATGAATCATTGATTGAATA 19
RESULT 41
3'-09-408-392-23
Sequence 23, Application US/09/408392
Patent No. 6376246
GENERAL INFORMATION:
APPLICANT: CRAMERI, ANDREAS
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: MINSHULL, JEREMY
APPLICANT: BASS, STEVEN H.
APPLICANT: WELCH, MARK
APPLICANT: NESS, JON E.
APPLICANT: GUSTAFSSON, CLAES
APPLICANT: PATTEN, PHILLIP A.
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
FILE REFERENCE: 02-029620US
CURRENT APPLICATION NUMBER: US/09/408,392
CURRENT FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 60/118,813
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 60/141,049
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
3'-09-408-392-23
Query Match 1.1%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1102 ATGAATCATTGATTGAATA 1120

Db 1 ATGAATCATTGATTGAATA 19
|||||
RESULT 42
US-09-626-930-23
Sequence 23, Application US/09626930
Patent No. 6423542
GENERAL INFORMATION:
APPLICANT: CRAMERI, ANDREAS
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: MINSHULL, JEREMY
APPLICANT: BASS, STEVEN H.
APPLICANT: WELCH, MARK
APPLICANT: NESS, JON E.
APPLICANT: GUSTAFSSON, CLAES
APPLICANT: PATTEN, PHILLIP A.
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
FILE REFERENCE: 02-029620US
CURRENT APPLICATION NUMBER: US/09/626,930
CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/408,392
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 60/118,813
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 60/141,049
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-626-930-23
Query Match 1.1%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1102 ATGAATCATTGATTGAATA 1120
|||||
1 ATGAATCATTGATTGAATA 19
Db 1 ATGAATCATTGATTGAATA 19
|||||
RESULT 43
US-09-626-528-23
Sequence 23, Application US/09626528
Patent No. 6426224
GENERAL INFORMATION:
APPLICANT: CRAMERI, ANDREAS
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: MINSHULL, JEREMY
APPLICANT: BASS, STEVEN H.
APPLICANT: WELCH, MARK
APPLICANT: NESS, JON E.
APPLICANT: GUSTAFSSON, CLAES
APPLICANT: PATTEN, PHILLIP A.
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
FILE REFERENCE: 02-029620US
CURRENT APPLICATION NUMBER: US/09/626,528
CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/408,392
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 60/118,813
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 60/141,049
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 19


```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
JS-09-626-528-23

Query Match      1.18; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 1102 ATGAATCATGATTGAATA 1120
|||||  |||  |||  |||  |||  |||
1 ATGAATAATGATTGAATA 19

RESULT 44
JS-09-626-595-23
; Sequence 23, Application US/09626595
; Patent No. 6479652
; GENERAL INFORMATION:
; APPLICANT: CRAMERI, ANDREAS
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: BASS, STEVEN H.
; APPLICANT: WELCH, MARK
; APPLICANT: NESS, JON E.
; APPLICANT: GUSTAFSSON, CLARS
; APPLICANT: PATTEN, PHILIP A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
; FILE REFERENCE: 02-029620US
; CURRENT APPLICATION NUMBER: US/09/626,595
; CURRENT FILING DATE: 2000-07-27
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 09/408,392
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/118,813
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/141,049
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
JS-09-626-595-23

Query Match      1.18; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 1102 ATGAATCATGATTGAATA 1120
|||||  |||  |||  |||  |||  |||
1 ATGAATAATGATTGAATA 19

RESULT 45
JS-09-694-863-23
; Sequence 23, Application US/09694863
; Patent No. 6521453
; GENERAL INFORMATION:
; APPLICANT: CRAMERI, ANDREAS
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: BASS, STEVEN H.
; APPLICANT: WELCH, MARK
; APPLICANT: NESS, JON E.
; APPLICANT: GUSTAFSSON, CLARS
; APPLICANT: PATTEN, PHILIP A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
; FILE REFERENCE: 02-029620US
; CURRENT APPLICATION NUMBER: US/09/694,863
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; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 09/408,392
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/141,049
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-694-863-23

Query Match      1.18; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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1 ATGAATAATGATTGAATA 19

RESULT 46
US-08-807-104-2
; Sequence 2, Application US/08807104
; Patent No. 5861501
; GENERAL INFORMATION:
; APPLICANT: BENSELER, FRITZ
; APPLICANT: COLE, JAMES L.
; APPLICANT: OLSEN, DAVID B.
; APPLICANT: KUO, LAWRENCE C.
; TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND
; TITLE OF INVENTION: APTAMERS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/807,104
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,068
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YABLONSKY, MICHAEL D
; REGISTRATION NUMBER: 40,407
; REFERENCE/DOCKET NUMBER: 19406DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-4678
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic RNA
; FEATURE:
; NAME/KEY: Modified Base
; LOCATION: 2...2
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OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 2...2
OTHER INFORMATION:
S-08-807-104-2

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 21.1%; Pred. No. 1.5e+02;
Matches 4; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

1519 GCTTTATATTTTAACTTT 1537
1 GGUUUUUUUUUUAUUU 19

35ULT 47
3-09-116-780-8
Sequence 8, Application US/09116780
Patent No. 5945335
GENERAL INFORMATION:
APPLICANT: COLOSL, Peter
TITLE OF INVENTION: Adenovirus Helper-Free Systems for Producing
TITLE OF INVENTION: Recombinant AAV Virions Lacking Oncogenic Sequences
FILE REFERENCE: 2555.2.2
CURRENT APPLICATION NUMBER: US/09/116,780
CURRENT FILING DATE: 1998-07-16
EARLIER APPLICATION NUMBER: 08/745,957
EARLIER FILING DATE: 1996-11-07
EARLIER APPLICATION NUMBER: 60/006,402
EARLIER FILING DATE: 1995-11-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide

S-09-116-780-8
Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

975 TGCGAAGCAGCTTAAAGTT 993
2 TGCGAAGCAGCTTAAAGTT 20

85ULT 48
S-08-480-068-2
Sequence 2, Application US/08480068
Patent No. 6111095
GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND APTAMERS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,068
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GIESSEY, JOANNE M
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19406
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3046
TELEFAX: 908-594-4720
TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Modified Base
LOCATION: 2...2
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 2...2
OTHER INFORMATION:
US-08-480-068-2

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 21.1%; Pred. No. 1.5e+02;
Matches 4; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

1519 GCTTTATATTTTAACTTT 1537
1 GGUUUUUUUUUUAUUU 19

RESULT 49
US-09-446-504-53
Sequence 53, Application US/09446504
Patent No. 6218150
GENERAL INFORMATION:
APPLICANT: UEMORI, Takashi
APPLICANT: SATO, Yoshiaki
APPLICANT: FUJITA, Tomoko
APPLICANT: MIYAKE, Kazuo
APPLICANT: MUKAI, Hiroyuki
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
FILE REFERENCE: 1422-408PCT
CURRENT APPLICATION NUMBER: US/09/446,504
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: JP 9-187496
PRIOR FILING DATE: 1997-06-26
PRIOR APPLICATION NUMBER: JP 9-320692
PRIOR FILING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 53
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA

; COMPUTER READABLE FORM:

SEQUENCE CHARACTERISTICS:

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LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

S-09-021-701-865

Query Match 1.1%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 982 GCACCTTAAGCTTTTTCAT 1000
 b 19 GCACCTTAAGCTTTTCCAT 1

RESULT 53

S-09-021-701-869/c
 Sequence 869, Application US/09021701
 Patent No. 6251588

GENERAL INFORMATION:

APPLICANT: Shannon, Karen W.
 APPLICANT: Wolber, Paul K.
 APPLICANT: Delenstarr, Glenda C.
 APPLICANT: Webb, Peter G.
 APPLICANT: Kincaid, Robert H.

TITLE OF INVENTION: Methods for evaluating oligonucleotide
 TITLE OF INVENTION: Probe sequences
 NUMBER OF SEQUENCES: 1165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
 STREET: 3000 Hanover Street
 CITY: Palo Alto
 STATE: CA

COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/021,701
 FILING DATE: 10-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Choi, Wendy A.

REGISTRATION NUMBER: 36,697

REFERENCE/DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-236-2386

TELEFAX: 650-852-8063

INFORMATION FOR SEQ ID NO: 869:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

S-09-021-701-869

Query Match 1.1%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 977 TCGAAGCACTTTAAGTTT 995
 b 20 TGGTTGCACCTTTAAATTT 2

RESULT 54

US-09-021-701-870/c

Sequence 870, Application US/09021701

Patent No. 6251588

GENERAL INFORMATION:

APPLICANT: Shannon, Karen W.

APPLICANT: Wolber, Paul K.

APPLICANT: Delenstarr, Glenda C.

APPLICANT: Webb, Peter G.

APPLICANT: Kincaid, Robert H.

TITLE OF INVENTION: Methods for evaluating oligonucleotide

TITLE OF INVENTION: Probe sequences

NUMBER OF SEQUENCES: 1165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
 STREET: 3000 Hanover Street
 CITY: Palo Alto
 STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/021,701

FILING DATE: 10-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Choi, Wendy A.

REGISTRATION NUMBER: 36,697

REFERENCE/DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-236-2386

TELEFAX: 650-852-8063

INFORMATION FOR SEQ ID NO: 870:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-021-701-870

Query Match 1.1%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 977 TCGAAGCACTTTAAGTTT 995

Db 19 TGGTTGCACCTTTAAATTT 1

RESULT 55

US-09-712-266-53

Sequence 53, Application US/09712266

Patent No. 6333158

GENERAL INFORMATION:

APPLICANT: UEMORI, Takashi

APPLICANT: SATO, Yoshiaki

APPLICANT: FUJITA, Tomoko

APPLICANT: MIYAKE, Kazuo

APPLICANT: MUKAI, Hiroyuki

APPLICANT: ASADA, Kiyozo

APPLICANT: KATO, Ikunoshin

TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS

FILE REFERENCE: 1422-408PCT

CURRENT APPLICATION NUMBER: US/09/712,266

CURRENT FILING DATE: 2000-11-15

PRIOR APPLICATION NUMBER: US 09/446,504
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: JP 9-187496
PRIOR FILING DATE: 1997-06-26
PRIOR APPLICATION NUMBER: JP 9-320692
PRIOR FILING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 53
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
JS-09-712-266-53

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2y 583 TACTTATATGTAAGTATT 601
db 1 TTCTGCTATGTAAGTATT 19

RESULT 56
US-09-712-266-54/c
Sequence 54, Application US/09712266
Patent No. 6333158
GENERAL INFORMATION:
APPLICANT: UEMORI, Takashi
APPLICANT: SATO, Yoshihimi
APPLICANT: FUJITA, Tomoko
APPLICANT: MIYAKE, Kazuo
APPLICANT: MUKAI, Hiroyuki
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
FILE REFERENCE: 1422-408PCT
CURRENT APPLICATION NUMBER: US/09/712,266
CURRENT FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 09/446,504
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: JP 9-187496
PRIOR FILING DATE: 1997-06-26
PRIOR APPLICATION NUMBER: JP 9-320692
PRIOR FILING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 54
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-712-266-54

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 583 TACTTATATGTAAGTATT 601
Db 20 TTCTGCTATGTAAGTATT 2

RESULT 57
US-08-973-137-2
Sequence 2, Application US/08973137

Patent No. 6369208
GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND APTAMERS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M. GIESSER - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,137
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,068
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: GIESSER, JOANNE M
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19406
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3046
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Modified Base
LOCATION: 2...2
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 2...2
OTHER INFORMATION:
US-08-973-137-2

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 21.1%; Pred. No. 1.5e+02;
Matches 4; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1519 GCTTTATATTTTAACTTT 1537
Db 1 GGUUUUUUUUUUUUU 19

RESULT 58
US-09-705-299-21
Sequence 21, Application US/09705299
Patent No. 6440737
GENERAL INFORMATION:
APPLICANT: Iex M. Cowsert
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR APOPTOSIS SUSCEPTIBILITY GENE
FILE REFERENCE: RTS-0174

CURRENT APPLICATION NUMBER: US/09/705,299
CURRENT FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 86
SEQ ID NO 21
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
-09-705-299-21

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1307 TGAATPACAACTCTAGTT 1325
1 TGAATPACAACTCTAGTT 19

ULT 59
09-668-313A-84/c
Sequence 84, Application US/09668313A
Patent No. 6503756
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF SYNTAXIN 4 INTERACTING PROTEIN EXPRESSION
FILE REFERENCE: RTS-0127
CURRENT APPLICATION NUMBER: US/09/668,313A
CURRENT FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 247
SEQ ID NO 84
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
09-668-313A-84

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1045 TATTATGATTTATTATTA 1063
19 TATTCTGTATACATTAA 1

ULT 60
09-198-452A-5710/c
Sequence 5710, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Grifflaib, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 5710
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
09-198-452A-5710

Query Match 1.1%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 968 GAGGACATGTGGAAGCACT 986
DB 19 GAGGATATTGGAAGCCCT 1

RESULT 61

US-08-311-486C-189
Sequence 189, Application US/08311486C
Patent No. 5811300
GENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kevin Kisich
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggan
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF-
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,486C
FILING DATE: September 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-311-486C-189

Query Match 1.1%; Score 14; DB 1; Length 15;
Best Local Similarity 28.6%; Pred. No. 77;
Matches 4; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1038 TATTATTTATTAT 1051
DB 1 UAUUUAUUUUUU 14

RESULT 62
US-08-311-486C-197
Sequence 197, Application US/08311486C

CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/311,486C
 FILING DATE: September 23, 1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA: including application
 PRIOR APPLICATION DATA: described below:
 APPLICATION NUMBER: 08/008,895
 FILING DATE: January 19, 1993
 APPLICATION NUMBER: 07/989,849
 FILING DATE: December 7, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 209/166
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 707:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 S-08-311-486C-707

Query Match 1.1%; Score 14; DB 1; Length 15;
 Best Local Similarity 28.6%; Pred. No. 77;
 Matches 4; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Y 1038 TATTATTATTAT 1051
 :|::|::|::|::|:
 1 UAUUUUUUUUUUU 14

RESULT 65
 S-08-311-486C-708
 Sequence 708, Application US/08311486C
 Patent No. 5811360
 GENERAL INFORMATION:
 APPLICANT: Sean Sullivan
 APPLICANT: Kenneth Draper
 APPLICANT: Kevin Kisich
 APPLICANT: Dan T. Stinchcomb
 APPLICANT: James McSwiggen
 TITLE OF INVENTION: RIBOZYME TREATMENT OF
 TITLE OF INVENTION: DISEASES OR CONDITIONS
 TITLE OF INVENTION: RELATED TO LEVELS OF
 TITLE OF INVENTION: TNF-
 NUMBER OF SEQUENCES: 1157
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible

two

OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/311,486C
 FILING DATE: September 23, 1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA: including application
 PRIOR APPLICATION DATA: described below:
 APPLICATION NUMBER: 08/008,895
 FILING DATE: January 19, 1993
 APPLICATION NUMBER: 07/989,849
 FILING DATE: December 7, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 209/166
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 708:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-311-486C-708

Query Match 1.1%; Score 14; DB 1; Length 15;
 Best Local Similarity 28.6%; Pred. No. 77;
 Matches 4; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1038 TATTATTATTAT 1051
 :|::|::|::|::|:
 Db 1 UAUUUUUUUUUUU 14

RESULT 66
 US-08-985-162-714
 Sequence 714, Application US/08985162
 Patent No. 6057156
 GENERAL INFORMATION:
 APPLICANT: Akhtar, Saghir
 APPLICANT: Fell, Patricia
 APPLICANT: McSwiggen, James
 TITLE OF INVENTION: ENZYMIC NUCLEIC ACID TREATMENT
 TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
 TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
 TITLE OF INVENTION: FACTOR RECEPTORS
 NUMBER OF SEQUENCES: 1877
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/985,162
 FILING DATE: 04 December 1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/036,476
 FILING DATE: 31 January 1997
 ATTORNEY/AGENT INFORMATION:

two


```
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 714:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-985-162-714

Query Match 1.1%; Score 14; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1599 AGTAAATATGAAC 1612
DB 2 AGTAAATATGAAC 15

RESULT 67
US-08-117-952-529/c
Sequence 529, Application US/08117952
Patent No. 5851760
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
APPLICANT: Smith, Michael W.
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9423
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 529:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Oligonucleotide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-117-952-529

Query Match 1.1%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 889 GTTCACATGTCCT 902
DB 17 GTTCACATGTCCT 4

RESULT 68
US-09-357-073-42
Sequence 42, Application US/09357073
Patent No. 6033910
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF MAP KINASE KINASE 6 EXPRESSION
FILE REFERENCE: RTS-0086
CURRENT APPLICATION NUMBER: US/09/357,073
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 42
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-073-42

Query Match 1.1%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1207 AAACAACACAA 1220
DB 7 AAACAACACAA 20

RESULT 69
US-09-198-452A-5776
Sequence 5776, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffois, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 5776
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5776

Query Match 1.1%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 644 TAAGGATTTTCCTA 657
DB 7 TAAGGATTTTCCTA 20

RESULT 70
US-08-373-124A-972/c
Sequence 972, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
```

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994

REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 972:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-373-124A-972

Query Match 1.1%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1615 TTAAATATATATTTT 1631
3 17 TAAATATATATTTT 1

RESULT 71
3-08-373-124A-2053/C
Sequence 2053, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles

STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 2053:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-373-124A-2053

Query Match 1.1%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1615 TTAAATATATATTTT 1631
Db 17 TAAATATATATTTT 1

RESULT 72
US-08-435-628-972/C
Sequence 972, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

```

CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/435,628
  FILING DATE: 05-MAY-1995
  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/373,124
  FILING DATE: January 13, 1995
  APPLICATION NUMBER: 08/245,466
  FILING DATE: May 18, 1994
  APPLICATION NUMBER: 08/192,943
  FILING DATE: February 7, 1994
  APPLICATION NUMBER: 07/987,132
  FILING DATE: December 7, 1992
  APPLICATION NUMBER: 07/936,422
  FILING DATE: August 26, 1992
  ATTORNEY/AGENT INFORMATION:
    NAME: Warburg, Richard
    REGISTRATION NUMBER: 32,327
    REFERENCE/DOCKET NUMBER: 209/035
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (213) 489-1600
      TELEFAX: (213) 955-0440
      TELEX: 67-3510
    INFORMATION FOR SEQ ID NO: 972:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 17 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
US-08-435-628-972

Query Match      1.1%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2Y 1615 TTAATAATATATTTGTT 1631
Db 17 TAAATAATATATTTT 1

RESULT 73
US-08-435-628-2053/c
  Sequence 2053, Application US/08435628
  Patent No. 5817796
  GENERAL INFORMATION:
    APPLICANT: Stinchcomb, Dan T.
    APPLICANT: Draper, Kenneth
    APPLICANT: McSwiggen, James
    APPLICANT: Jarvis, Thale
    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
    TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
    TITLE OF INVENTION: CANCER USING RIBOZYMES
    NUMBER OF SEQUENCES: 2627
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Lyon & Lyon
      STREET: 633 West Fifth Street
      STREET: Suite 4700
      CITY: Los Angeles
      STATE: California
      COUNTRY: U.S.A.
      ZIP: 90071
    COMPUTER READABLE FORM:
      MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
      MEDIUM TYPE: storage
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: IBM P.C. DOS 5.0
    SOFTWARE: Word Perfect 5.1
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/435,628
      FILING DATE: 05-MAY-1995
      CLASSIFICATION: 514
      PRIOR APPLICATION NUMBER: 08/373,124

```

```

  FILING DATE: January 13, 1995
  APPLICATION NUMBER: 08/245,466
  FILING DATE: May 18, 1994
  APPLICATION NUMBER: 08/192,943
  FILING DATE: February 7, 1994
  APPLICATION NUMBER: 07/987,132
  FILING DATE: December 7, 1992
  APPLICATION NUMBER: 07/936,422
  FILING DATE: August 26, 1992
  ATTORNEY/AGENT INFORMATION:
    NAME: Warburg, Richard
    REGISTRATION NUMBER: 32,327
    REFERENCE/DOCKET NUMBER: 209/035
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (213) 489-1600
      TELEFAX: (213) 955-0440
      TELEX: 67-3510
    INFORMATION FOR SEQ ID NO: 2053:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 17 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
US-08-435-628-2053

Query Match      1.1%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1615 TTAATAATATATTTGTT 1631
Db 17 TAAATAATATATTTT 1

RESULT 74
US-09-468-265-23
  Sequence 23, Application US/09468265
  Patent No. 6379928
  GENERAL INFORMATION:
    APPLICANT: Berka, Randy M
    APPLICANT: Cullen, Daniel
    APPLICANT: Gray, Gregory L
    APPLICANT: Hayerga, Kirk J
    APPLICANT: Lawlis, Virgil B
    TITLE OF INVENTION: Heterologous Polypeptides Expressed in Filamentous Fungi, Proces
    TITLE OF INVENTION: Making Same and Vectors for Making Same
    FILE REFERENCE: A-42309-5
    CURRENT APPLICATION NUMBER: US/09/468,265
    CURRENT FILING DATE: 1999-12-10
    PRIOR APPLICATION NUMBER: 08/484,384
    PRIOR FILING DATE: 1995-06-07
    PRIOR APPLICATION NUMBER: 08/284,942
    PRIOR FILING DATE: 1994-08-02
    PRIOR APPLICATION NUMBER: 07/413,010
    PRIOR FILING DATE: 1989-09-25
    PRIOR APPLICATION NUMBER: 07/163,219
    PRIOR FILING DATE: 1988-02-26
    PRIOR APPLICATION NUMBER: 06/882,224
    PRIOR FILING DATE: 1986-07-07
    PRIOR APPLICATION NUMBER: 06/771,374
    PRIOR FILING DATE: 1985-08-29
    NUMBER OF SEQ ID NOS: 28
    SOFTWARE: Patent in version 3.1
    SEQ ID NO 23
    LENGTH: 17
    TYPE: DNA
    ORGANISM: Artificial Sequence
    FEATURE:
      OTHER INFORMATION: synthetic oligonucleotide probes
US-09-468-265-23

Query Match      1.1%; Score 13.8; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;

```


ATTORNEY/AGENT INFORMATION:
NAME: Gieser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19393
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)-594-3046
TELEFAX: (908)-594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-759-1

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

Y 1521 TTTATATTTTAACTTT 1537
DB 2 UUUUUAUUUUUAUUU 18

RESULT 79
US-08-807-104-1
Sequence 1, Application US/08807104
Patent No. 5861501
GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPED SYNTHETIC RNA, ANALOGS, AND
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,104
FILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,068
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YABLONSKY, MICHAEL D
REGISTRATION NUMBER: 40,407
REFERENCE/DOCKET NUMBER: 19406DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4678
TELEFAX: 732-594-4720
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
FEATURE:

NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
US-08-807-104-1

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;
QY 1521 TTTATATTTTAACTTT 1537
DB 2 UUUUUAUUUUUAUUU 18

RESULT 80
US-08-807-104-4
Sequence 4, Application US/08807104
Patent No. 5861501
GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPED SYNTHETIC RNA, ANALOGS, AND
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,104
FILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,068
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YABLONSKY, MICHAEL D
REGISTRATION NUMBER: 40,407
REFERENCE/DOCKET NUMBER: 19406DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4678
TELEFAX: 732-594-4720
TELEX:

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
FEATURE:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
US-08-807-104-4

Query Match 1.1%; Score 13.8; DB 1; Length 19;

Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

Y 1521 TTATATTTTAACTTT 1537
2 UUUUUUUUUUUUUUUU 18

RESULT 81

3-08-807-104-6
Sequence 6, Application US/08807104
Patent No. 5861501
GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: MICHAEL D. YABLONSKY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807.104
FILING DATE: 04-FEB-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,068

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: YABLONSKY, MICHAEL D

REGISTRATION NUMBER: 40,407

REFERENCE/DOCKET NUMBER: 19406DA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-4678

TELEFAX: 732-594-4720

TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic RNA

FEATURE:

NAME/KEY: Modified Base

LOCATION: 1...1

OTHER INFORMATION:

NAME/KEY: Modified Base

LOCATION: 1...1

OTHER INFORMATION:

NAME/KEY: Modified Base

LOCATION: 13...13

OTHER INFORMATION:

3-08-807-104-6

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

Y 1521 TTATATTTTAACTTT 1537
2 UUUUUUUUUUUUUUUU 18

RESULT 83

US-08-807-104-8
; Sequence 8, Application US/08807104
; Patent No. 5861501

RESULT 82

US-08-807-104-7
; Sequence 7, Application US/08807104
; Patent No. 5861501
; GENERAL INFORMATION:

APPLICANT: BENSELER, FRITZ

APPLICANT: COLE, JAMES L.

APPLICANT: OLSEN, DAVID B.

APPLICANT: KUO, LAWRENCE C.

TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND

TITLE OF INVENTION: APTAMERS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSER: MICHAEL D. YABLONSKY - MERCK & CO., INC.

STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000

CITY: RAHWAY

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/807.104

FILING DATE: 04-FEB-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/480,068

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: YABLONSKY, MICHAEL D

REGISTRATION NUMBER: 40,407

REFERENCE/DOCKET NUMBER: 19406DA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-4678

TELEFAX: 732-594-4720

TELEX:

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic RNA

FEATURE:

NAME/KEY: Modified Base

LOCATION: 1...1

OTHER INFORMATION:

NAME/KEY: Modified Base

LOCATION: 1...1

OTHER INFORMATION:

NAME/KEY: Modified Base

LOCATION: 13...13

OTHER INFORMATION:

US-08-807-104-7

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 1521 TTATATTTTAACTTT 1537

2 UUUUUUUUUUUUUUUU 18

RESULT 83

US-08-807-104-8
; Sequence 8, Application US/08807104
; Patent No. 5861501

GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,104
FILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,068
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YABLONSKY, MICHAEL D
REGISTRATION NUMBER: 40,407
REFERENCE/DOCKET NUMBER: 19406DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4678
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
FEATURE:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 6...6
OTHER INFORMATION:
US-08-807-104-8
Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 1521 TTTATATTTTAACTTT 1537
:::|:|||||:::
Db 2 UUUUUUUUUUUUUUU 18

RESULT 84
US-08-807-104-9
Sequence 9, Application US/08807104
Patent No. 5861501
GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND

GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,104
FILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,068
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YABLONSKY, MICHAEL D
REGISTRATION NUMBER: 40,407
REFERENCE/DOCKET NUMBER: 19406DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4678
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
FEATURE:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 6...6
OTHER INFORMATION:
US-08-807-104-9
Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 1521 TTTATATTTTAACTTT 1537
:::|:|||||:::
Db 2 UUUUUUUUUUUUUUU 18

RESULT 85
US-08-807-104-10
Sequence 10, Application US/08807104
Patent No. 5861501
GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY

```

Query Match          1.18; Score 13.8; DB 1; Length 19;
Best local Similarity 17.68; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels

Y      1521 TTTATATTTTAACTTT 1537
D      2 UUUUUUUUUUUUUUUUU 18

          ::::|:::|:::|
          2 UUUUUUUUUUUUUUUUU 18

RESULT 86
3-08-807-104-13
Sequence 13, Application US/08807104
Patent No. 5861501
GENERAL INFORMATION:
  APPLICANT: BENSELER, FRITZ
  APPLICANT: COLE, JAMES L.
  APPLICANT: OLSEN, DAVID B.
  APPLICANT: KUO, LAWRENCE C.
  TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND
  NUMBER OF INVENTION: APTAMERS
  NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
  ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.
  STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
  CITY: RAYHAW
  STATE: NJ
  COUNTRY: USA
  ZIP: 07065
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette
  COMPUTER: IBM Compatible

```


REFERENCE/DOCKET NUMBER: 19406DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4678
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
FEATURE:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 2...2
OTHER INFORMATION:
US-08-807-104-14

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

2Y 1521 TTTATATTTTAACTTT 1537
+++|++++|+++
2 UUUUUUUUUUUUUUUU 18

2B

RESULT 88
US-08-807-104-15
Sequence 15, Application US/08807104
Patent No. 5861501
GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,104
FILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,068
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YABLONSKY, MICHAEL D
REGISTRATION NUMBER: 40,407
REFERENCE/DOCKET NUMBER: 19406DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4678
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
FEATURE:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 13...13
OTHER INFORMATION:
US-08-807-104-15

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 1521 TTTATATTTTAACTTT 1537
+++|++++|+++
2 UUUUUUUUUUUUUUUU 18

DB

RESULT 89
US-08-807-104-16
Sequence 16, Application US/08807104
Patent No. 5861501
GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,104
FILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,068
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YABLONSKY, MICHAEL D
REGISTRATION NUMBER: 40,407
REFERENCE/DOCKET NUMBER: 19406DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4678
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA

```

FEATURE:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 12...12
OTHER INFORMATION:
S-08-807-104-16
Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;
y 1521 TTTATATTITTAACCTT 1537
:: :|:||||| ::
b 2 UUUUUAUUUUAAUUU 18

RESULT 90
S-08-973-139-1
Sequence 1, Application US/08973139
Patent No. 6100028
GENERAL INFORMATION:
APPLICANT: Cole, James L.
APPLICANT: Olsen, David B.
APPLICANT: Kuo, Lawrence C.
TITLE OF INVENTION: DNA POLYMERASE EXTENSION ASSAY
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Ms. Joanne J. Giesser
STREET: 126 E. Lincoln Avenue, P.O. Box 2000-0907
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,139
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/487,760
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Giesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19398
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)-594-3046
TELEFAX: (908)-594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
US-08-973-139-1
Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;
y 1521 TTTATATTITTAACCTT 1537
:: :|:||||| ::
b 2 UUUUUAUUUUAAUUU 18

FEATURE:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 12...12
OTHER INFORMATION:
S-08-807-104-16
Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;
y 1521 TTTATATTITTAACCTT 1537
:: :|:||||| ::
b 2 UUUUUAUUUUAAUUU 18

RESULT 91
US-08-480-068-1
Sequence 1, Application US/08480068
Patent No. 611095
GENERAL INFORMATION:
APPLICANT: BENSLER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND APTAMERS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M. GIESSER - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,068
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GIESSER, JOANNE M
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19406
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3046
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
US-08-480-068-1
Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;
y 1521 TTTATATTITTAACCTT 1537
:: :|:||||| ::
b 2 UUUUUAUUUUAAUUU 18

RESULT 92
US-08-480-068-4
Sequence 4, Application US/08480068

```

Patent No. 6111095
GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND APTAMERS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,068
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GIESSEY, JOANNE M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19406
TELEPHONE: 908-594-3046
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
US-08-480-068-4
Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;
QY 1521 TTTATATTTTAACTTT 1537
Db 2 UUUUUUUUUUUUUUU 18
RESULT 93
US-08-480-068-6
Sequence 6, Application US/08480068
Patent No. 6111095
GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND APTAMERS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND APTAMERS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,068
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GIESSEY, JOANNE M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19406
TELEPHONE: 908-594-3046
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 13...13
OTHER INFORMATION:
US-08-480-068-6
Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;
QY 1521 TTTATATTTTAACTTT 1537
Db 2 UUUUUUUUUUUUUUU 18
RESULT 94
US-08-480-068-7
Sequence 7, Application US/08480068
Patent No. 6111095
GENERAL INFORMATION:
APPLICANT: BENSELER, FRITZ
APPLICANT: COLE, JAMES L.
APPLICANT: OLSEN, DAVID B.
APPLICANT: KUO, LAWRENCE C.
TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND APTAMERS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:


```
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 12...12
OTHER INFORMATION:
US-08-480-068-15
Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

>Y 1521 TTTATATTTTAACTTT 1537
::: ||::||::|
>b 2 UUUUUUUUUUUUUU 18

RESULT 101
US-08-480-068-16
; Sequence 16, Application US/08480068
; Patent No. 611095
; GENERAL INFORMATION:
; APPLICANT: BENSELER, FRITZ
; APPLICANT: COLE, JAMES L.
; APPLICANT: OLSEN, DAVID B.
; APPLICANT: KUO, LAWRENCE C.
; TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND APTAMERS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOANNE M. GLESSER - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/480,068
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: GLESSER, JOANNE M
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 19406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3046
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:

TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 1...1
OTHER INFORMATION:
NAME/KEY: Modified Base
LOCATION: 13...13
OTHER INFORMATION:
US-08-480-068-16
Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

>Y 1521 TTTATATTTTAACTTT 1537
::: ||::||::|
>b 2 UUUUUUUUUUUUUU 18

RESULT 102
US-08-973-137-1
; Sequence 1, Application US/08973137
; Patent No. 6369208
; GENERAL INFORMATION:
; APPLICANT: BENSELER, FRITZ
; APPLICANT: COLE, JAMES L.
; APPLICANT: OLSEN, DAVID B.
; APPLICANT: KUO, LAWRENCE C.
; TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND APTAMERS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOANNE M. GLESSER - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/973,137
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,068
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GLESSER, JOANNE M
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 19406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3046
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
```



```

matcheb 5; counselvative 127; nlemaclucches 4; lnuclab 6; oagys 0
QY 1521 TTTATATTTTTTAACCTT 1537
::: :|:::|:::|
db 2 UUUUUUUUUUUUUUUUU 18

```

RESULT 108
US-08-973-137-10
; Sequence 10, Application US/08973137
; Patent No. 6369208
; GENERAL INFORMATION:
; APPLICANT: BENSELER, FRITZ
; APPLICANT: COLE, JAMES L.
; APPLICANT: OLSEN, DAVID B.
; APPLICANT: KIO, LAWRENCE C.
; TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND APTAMERS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOANNE M. GIESSEY & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,137
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/480,068
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: GIESSER, JOANNE M
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19406
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3046
TELEFAX: 908-594-4720
TELEX:

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1 INFORMATION FOR SEQ ID NO: 10:
2 SEQUENCE CHARACTERISTICS:
3     LENGTH: 19 base pairs
4     TYPE: nucleic acid
5     STRANDEDNESS: single
6     TOPOLOGY: linear
7     MOLECULE TYPE: Genomic RNA
8     HYPOTHETICAL: NO
9     ANTI-SENSE: NO
10    FRAGMENT TYPE:
11    ORIGINAL SOURCE:
12    FEATURE:
13    NAME/KEY: Modified Base
14    LOCATION: 1...1
15    OTHER INFORMATION:
16    NAME/KEY: Modified Base
17    LOCATION: 1...1
18    OTHER INFORMATION:
19    NAME/KEY: Modified Base
20    LOCATION: 19...19
21    OTHER INFORMATION:
22 US-08-973-137-10

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Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 17.6%; Pred. No. 1.7e+02;
Matches 3; Conservative 12; Mismatches 2; Indels

Db :::|:||||:| :::
2 UUUUUUUUUUUUUUUU 18

RESULT 109

JS-08-973-137-13

; Sequence 13, Application US/08973137

; Patent No. 6369208

; GENERAL INFORMATION:

; APPLICANT: BENSELER, FRITZ

; APPLICANT: COLE, JAMES L.

; APPLICANT: OLSEN, DAVID B.

; APPLICANT: KUO, LAWRENCE C.

; TITLE OF INVENTION: CAPPED SYNTHETIC RNA, ANALOGS, AND APTAMERS

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.

; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000

; CITY: RAHWAY

; STATE: NJ

; COUNTRY: US

; ZIP: 07065-0907

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/973,137

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/480,068

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: GIESSEY, JOANNE M.

; REGISTRATION NUMBER: 32,838

; REFERENCE/DOCKET NUMBER: 19406

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 908-594-3046

; TELEFAX: 908-594-4720

; TELEX:

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Genomic RNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE:

; ORIGINAL SOURCE:

; FEATURE:

; NAME/KEY: Modified Base

; LOCATION: 1...1

; OTHER INFORMATION:

; JS-08-973-137-13

Query Match

Best Local Similarity 17.6%; Score 13.8; DB 1; Length 19;

Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

Yy 1521 TTTATATTTTAACTTT 1537

:::|:||||:| :::

2 UUUUUUUUUUUUUUUU 18

RESULT 110

JS-08-973-137-14

; Sequence 14, Application US/08973137

; Patent No. 6369208

; GENERAL INFORMATION:

; APPLICANT: BENSELER, FRITZ

; APPLICANT: COLE, JAMES L.

; APPLICANT: OLSEN, DAVID B.

APPLICATION NUMBER: US/08/973.137

INFORMATION FOR THE...

LENGTH: 19 base pairs

COMMISSIONER OF REVENUE
P.O. STATOVI: 7411

PREPARED BY: BRIGIO
 TODAY ONLY. 11:00 AM

MOLECULAR TYPE. Genomic B

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

THE UNIVERSITY OF CHICAGO

LOCATION: 1 1

OTHER INFORMATION:

NAME/KEY: Modified Bas

LOCATION: 1...1

OTHER INFORMATION:

NAME/REF:	MODIFIED	DATE
1000000000	10	10

OTHER INFORMATION:

-973-137-16

1.1

Local Similarity 17.6

DATE RECEIVED, 1967

1521 ԴԱՏԱՐ ԺԱՅ Զ ԴԱՏԱՐԱՐՈՒՄ Զ ԸՆԴՈՒՄ

[illegible]

2. 2000A JOURNAL OF CLIMATE

CTT

[illegible]

CONF No 6537757

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

PLACANT: CHUMAKOV, ILYA

***** NOT IN A *****

REPORT ADDITION NUMBER:

CURRENT FILING DATE. 1999-10-

LIBR APPLICATION NUMBER:

LIBR FILING DATE: 1999-04

EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 8817
LENGTH: 19
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..19
OTHER INFORMATION: downstream amplification primer 99-18438 for SEQ 952, in complete
US-09-422-978-8817

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DY 1208 AACAAACAACAATGG 1224
|||||
DB 1 AACAAACAACAAC TAG 17

RESULT 114
PCT-US93-02259-7

Sequence 7, Application PC/TUS9302259
GENERAL INFORMATION:
APPLICANT: Fortina, Paolo
TITLE OF INVENTION: DIAGNOSIS OF CYSTIC FIBROSIS USING
TELECOMMUNICATION INFORMATION: CH-0224
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02259
FILING DATE: 19930311

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, Philip S.
REGISTRATION NUMBER: 27,200
REFERENCE/DOCKET NUMBER: CH-0224
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

PCT-US93-02259-7

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DY 1435 AATTCTTGCTGGTTGA 1451
|||||
DB 2 AATTCTTGCTGGTTGA 18

RESULT 115

PCT-US93-02259-8
Sequence 8, Application PC/TUS9302259
GENERAL INFORMATION:
APPLICANT: Fortina, Paolo
TITLE OF INVENTION: DIAGNOSIS OF CYSTIC FIBROSIS USING
TELECOMMUNICATION INFORMATION: CH-0224
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02259
FILING DATE: 19930311

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Johnson, Philip S.
REGISTRATION NUMBER: 27,200
REFERENCE/DOCKET NUMBER: CH-0224
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

PCT-US93-02259-8

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DY 1435 AATTCTTGCTGGTTGA 1451
|||||
DB 2 AATTCTTGCTGGTTGA 18

RESULT 116

PCT-US96-08320-1
Sequence 1, Application PC/TUS9608320
GENERAL INFORMATION:
APPLICANT: Cole, James L.
APPLICANT: Olsen, David B.
TITLE OF INVENTION: DNA POLYMERASE EXTENSION ASSAY FOR
INFLUENZA VIRUS ENDONUCLEASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ms. Joanne J. Gieser
STREET: 126 E. Lincoln Avenue, P.O. Box 2000-0907
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

Query Match 1.1%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DY 1435 AATTCTTGCTGGTTGA 1451
|||||
DB 2 AATTCTTGCTGGTTGA 18

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32, 838
REFERENCE/DOCKET NUMBER: 19398 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)-594-3046
TELEFAX: (908)-594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
TT-US96-08330-1

RESULT 119
US-08-123-449A-2
; Sequence 2, Application US/08123449A
; Patent No. 5583032
; GENERAL INFORMATION:

```

; APPLICANT: TORRENCE, PAUL
; APPLICANT: ROBERT, SILVERMAN
; APPLICANT: RATAN, MAITRA
; APPLICANT: KRISTYNA, LESIAK
; TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
; TITLE OF INVENTION: OF RNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS version
; SOFTWARE: FastSeq Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,449A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10103
; FILING DATE: 10-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH034.001QPC
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
;
; US-08-123-449A-2
;
; Query Match 1.1%; Score 13.6; DB 1; Length 22;
; Best Local Similarity 80.0%; Pred. No. 2.8e+02;
; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
;
QY 1560 AAATTTTCTTCTTCT 1579
Db 2 AAATTTTCTTCTTCT 21
;
; RESULT 120
; US-08-458-050-1
; Sequence 1, Application US/08458050
; Patent No. 5677289
; GENERAL INFORMATION:
; APPLICANT: TORRENCE, PAUL
; APPLICANT: ROBERT, SILVERMAN
; APPLICANT: RATAN, MAITRA
; APPLICANT: KRISTYNA, LESIAK
; TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
; TITLE OF INVENTION: OF RNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS version
; SOFTWARE: FastSeq Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,050
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,449
; FILING DATE: 17-SEP-1993
; APPLICATION NUMBER: PCT/US93/10103
; FILING DATE: 10-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH034.001QPC
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
;
; US-08-458-050-1
;
; Query Match 1.1%; Score 13.6; DB 1; Length 22;
; Best Local Similarity 80.0%; Pred. No. 2.8e+02;
; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
;
QY 1560 AAATTTTCTTCTTCT 1579
Db 2 AAATTTTCTTCTTCT 21
;
; RESULT 121
; US-08-458-050-2
; Sequence 2, Application US/08458050
; Patent No. 5677289
; GENERAL INFORMATION:
; APPLICANT: TORRENCE, PAUL
; APPLICANT: ROBERT, SILVERMAN
; APPLICANT: RATAN, MAITRA
; APPLICANT: KRISTYNA, LESIAK
; TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
; TITLE OF INVENTION: OF RNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS version
; SOFTWARE: FastSeq Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,050
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,449

```

```

/ LENGTH: 22 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ US-08-950-196-1
/
Query Match 1.1%; Score 13.6; DB 1; Length 22;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1560 AAATTTTTTACTGTTCT 1579
Db 2 AAATTTTTTTTTTTTTT 21

RESULT 123
US-08-950-196-2
/ Sequence 2, Application US/08950196
/ Patent No. 6271369
/ GENERAL INFORMATION:
/ APPLICANT: TORRENCE, PAUL
/ APPLICANT: ROBERT, SILVERMAN
/ APPLICANT: RAYAN, MAITRA
/ APPLICANT: KRISTYNA, LESIAK
/ TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
/ TYPE OF INVENTION: OF RNA
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: Knobbe, Martens, Olson and Bear
/ STREET: 620 Newport Center Drive
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 92660
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS version
/ SOFTWARE: FastSeq Version 1.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/950,196
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/123,449
/ FILING DATE:
/ APPLICATION NUMBER: PCT/US93/10103
/ FILING DATE: 10-OCT-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pedrick, Michael P.
/ REGISTRATION NUMBER: 36,799
/ REFERENCE/DOCKET NUMBER: NIH034.001QPC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 714-760-0404
/ TELEFAX: 714-760-9502
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ US-08-950-196-2
/
Query Match 1.1%; Score 13.6; DB 1; Length 22;

```


Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1560 AAAATTTTCTAGTCTCT 1579
|||||
2 AAAATTTTCTTTTCTTT 21

RESULT 124

3-08-242-402-5/c
Sequence 5, Application US/08242402
Patent No. 5580967

GENERAL INFORMATION:
APPLICANT: JOYCE, GERALD F
TITLE OF INVENTION: OPTIMIZED CATALYTIC DNA-CLEAVING
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE, OFFICE OF
ADDRESS: PATENT COUNSEL
STREET: 10666 NORTH TORREY PINES ROAD, TPC 8
CITY: LA JOLLA
STATE: CA

COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/242,402
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LOGAN, APRIL C
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: TSRI 412.0
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-242-402-5

Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1047 TTTATGTTATTTATTT 1061
Db 15 TTTATTTATTTATTT 1

RESULT 125

US-08-242-402-21
Sequence 21, Application US/08242402
Patent No. 5580967

GENERAL INFORMATION:
APPLICANT: JOYCE, GERALD F
TITLE OF INVENTION: OPTIMIZED CATALYTIC DNA-CLEAVING
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE, OFFICE OF
ADDRESS: PATENT COUNSEL
STREET: 10666 NORTH TORREY PINES ROAD, TPC 8
CITY: LA JOLLA
STATE: CA

STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,402
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LOGAN, APRIL C
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: TSRI 412.0
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-242-402-21

Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1047 TTTATGTTATTTATTT 1061
Db 1 TTTATTTATTTATTT 15

RESULT 126

US-08-270-180-6
Sequence 6, Application US/08270180
Patent No. 5595873

GENERAL INFORMATION:
APPLICANT: JOYCE, GERALD F
TITLE OF INVENTION: ENZYMIC RNA MOLECULES THAT CLEAVE
TITLE OF INVENTION: AMIDE BONDS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 5595873th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/270,180
FILING DATE: 01-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,402
FILING DATE: 13-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: TSRI 412.1
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

QY 1047 TTTATGTTATTTATTT 1061
Db 15 TTTATTTATTTATTT 15

RESULT 126

US-08-270-180-6
Sequence 6, Application US/08270180
Patent No. 5595873

GENERAL INFORMATION:
APPLICANT: JOYCE, GERALD F
TITLE OF INVENTION: ENZYMIC RNA MOLECULES THAT CLEAVE
TITLE OF INVENTION: AMIDE BONDS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 5595873th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/270,180
FILING DATE: 01-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,402
FILING DATE: 13-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: TSRI 412.1
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3-08-270-180-6

Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1047 TTATTATTTATTT 1061
|||||
1 TTATTATTTATTT 15

RESULT 127
3-08-311-486C-190
Sequence 190, Application US/08311486C
Patent No. 5811300
GENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kevin Kisich
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF-
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,486C
FILING DATE: September 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/166
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
3-08-311-486C-190

two

Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 26.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

1039 ATTATTATTTATGT 1053
|||||
1 ATTATTAUUUUUUU 15

RESULT 128
US-08-311-486C-191
Sequence 191, Application US/08311486C
Patent No. 5811300
GENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kevin Kisich
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF-
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,486C
FILING DATE: September 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/166
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-311-486C-191

two

Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 26.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

1041 TTATTATTTATGTAT 1055
|||||
1 UUUUUUUUUUUUU 15

```

Query Match      1.18; Score 13.4; DB 1; Length 15;
Best Local Similarity 26.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1039 ATTATTATTATTATGT 1053
|:::|::|::|::|::|
1 AUUUUUUUUUUUUU 15

```

LT 131
B-311-486C-199
Sequence 199, Application US/06311486C
Inventor No. 5811300
GENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kevin Kisich
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwigen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
RELATED TO LEVELS OF
TNF- α

Applicant No. 5811300
 GENERAL INFORMATION:
 APPLICANT: Sean Sullivan
 APPLICANT: Kenneth Draper
 APPLICANT: Kevin Kisch
 APPLICANT: Dan T. Stinchcomb
 APPLICANT: James McSwiggen
 TITLE OF INVENTION: RIBOZYME TREATMENT OF
 TITLE OF INVENTION: DISEASES OR CONDITIONS
 TITLE OF INVENTION: RELATED TO LEVELS OF
 TITLE OF INVENTION: TNF- α

TOPOLOGY: Linear

00
1091 111111111111 1033

1041 TTATTATTATGTAT 1055

QY 1041 TTATTATTATGTAT 1055
 ::||::||::||::||::

Db 1 UUAUUAUUUUUU 15

RESULT 138

US-08-311-486C-713
; Sequence 713, Application US/08311486C
; Patent No. 5811300

GENERAL INFORMATION:
; APPLICANT: Sean Sullivan

APPLICANT: Kenneth Draper

APPLICANT: Kevin Kisich

APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen

TITLE OF INVENTION: RIBOZYME TREATMENT OF

TITLE OF INVENTION: DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF

TITLE OF INVENTION: TNF-

NUMBER OF SEQUENCES: 1157

CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/311,486C

FILING DATE: September 23, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/008,895

FILING DATE: January 19, 1993

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/166

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 713:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-311-486C-713

Query Match 1.1%; Score 13.4; DB 1; Length 15;

Best Local Similarity 26.7%; Pred. No. 1.1e+02;

Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1041 TTATTATTATGTAT 1055

Db 1 UUAUUAUUUUUU 15

RESULT 139

US-08-311-486C-714
; Sequence 714, Application US/08311486C
; Patent No. 5811300

GENERAL INFORMATION:
; APPLICANT: Sean Sullivan

APPLICANT: Kenneth Draper

APPLICANT: Kevin Kisich

APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen

TITLE OF INVENTION: RIBOZYME TREATMENT OF

TITLE OF INVENTION: DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF

TITLE OF INVENTION: TNF-

NUMBER OF SEQUENCES: 1157

CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/311,486C

FILING DATE: September 23, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/008,895

FILING DATE: January 19, 1993

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/166

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 713:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-311-486C-713

Query Match 1.1%; Score 13.4; DB 1; Length 15;

Best Local Similarity 26.7%; Pred. No. 1.1e+02;

Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1041 TTATTATTATGTAT 1055

Db 1 UUAUUAUUUUUU 15

APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kevin Kisich
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen

TITLE OF INVENTION: RIBOZYME TREATMENT OF

TITLE OF INVENTION: DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF

TITLE OF INVENTION: TNF-

NUMBER OF SEQUENCES: 1157

CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/311,486C

FILING DATE: September 23, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/008,895

FILING DATE: January 19, 1993

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/166

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 714:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-311-486C-714

Query Match 1.1%; Score 13.4; DB 1; Length 15;

Best Local Similarity 26.7%; Pred. No. 1.1e+02;

Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1041 TTATTATTATGTAT 1055

Db 1 UUAUUAUUUUUU 15

RESULT 140

US-08-311-486C-715
; Sequence 715, Application US/08311486C
; Patent No. 5811300

GENERAL INFORMATION:
; APPLICANT: Sean Sullivan

APPLICANT: Kenneth Draper

APPLICANT: Kevin Kisich

APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen

TITLE OF INVENTION: RIBOZYME TREATMENT OF

TITLE OF INVENTION: DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF

TITLE OF INVENTION: TNF-

NUMBER OF SEQUENCES: 1157

CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/311,486C

FILING DATE: September 23, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/008,895

FILING DATE: January 19, 1993

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/166

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 714:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-311-486C-714

two

two

Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 26.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 10; Mismatches 1; Indels

RESULT 142
US-08-311-486C-721
; Sequence 721, Application US/08311486C
; Patent No. 5811300
; GENERAL INFORMATION:

```

? APPLICANT: Kevin Kisch
?
? APPLICANT: Dan T. Stinchcomb
?
? APPLICANT: James McSwiggen
?
? TITLE OF INVENTION: RIBOZYME TREATMENT OF
?
? TITLE OF INVENTION: DISEASES OR CONDITIONS
?
? TITLE OF INVENTION: RELATED TO LEVELS OF
?
? TITLE OF INVENTION: TNP-1
?
? NUMBER OF SEQUENCES: 1157
?
? CORRESPONDENCE ADDRESSES:
?
? ADDRESSEE: Lyon & Lyon
?
? STREET: 633 West Fifth Street
?
? STREET: Suite 4700
?
? CITY: Los Angeles
?
? STATE: California
?
? COUNTRY: U.S.A.
?
? ZIP: 90071-2066
?
? COMPUTER READABLE FORM:
?
? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
?
? MEDIUM TYPE: storage
?
? COMPUTER: IBM Compatible
?
? OPERATING SYSTEM: IBM P.C. DOS 5.0
?
? SOFTWARE: Word Perfect 5.1
?

```


;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/311,486C
;; FILING DATE: September 23, 1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA: including application
;; PRIOR APPLICATION DATA: described below:
;; APPLICATION NUMBER: 08/008,895
;; FILING DATE: January 19, 1993
;; APPLICATION NUMBER: 07/989,849
;; FILING DATE: December 7, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 209/166
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 721:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; TWO

Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 26.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1043 ATTATTATGTTT 1057
Db 1 AUAUAUAUAUAUU 15

RESULT 143
US-08-500-635A-13/c
; Sequence 13, Application US/08500635A
; Patent No. 5955072
; GENERAL INFORMATION:
; APPLICANT: TAKAHASHI, Tohru
; APPLICANT: SERIZAWA, No. 5955072ufusa
; APPLICANT: KOISHI, Ryuta
; APPLICANT: KAWASHIMA, Ichiro
; TITLE OF INVENTION: EXPRESSION SYSTEMS UTILIZING
; TITLE OF INVENTION: AUTOLYZING FUSION PROTEINS
; TITLE OF INVENTION: AND A NOVEL REDUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frishauf, Holtz, Goodman, Langer & Chick, P.C.
; STREET: 767 Third Avenue-25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10017-2023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500,635A
; FILING DATE: 11-JUL-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-161053
; FILING DATE: 13-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-218392
; FILING DATE: 13-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-303809

;; FILING DATE: 07-DEC-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goodman, Herbert
;; REGISTRATION NUMBER: 17081
;; REFERENCE/DOCKET NUMBER: 950376/HG
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 319-4900
;; TELEFAX: (212) 319-5101
;; TELEX: 236268
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid, synthetic DNA
;; HYPOTHETICAL: N
;; ANTI-SENSE: N
;; US-08-500-635A-13

Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1044 TTATTATGTTT 1058
Db 15 TTATTATTATT 1

RESULT 144
US-08-682-423-6
; Sequence 6, Application US/08682423
; Patent No. 6063566
; GENERAL INFORMATION:
; APPLICANT: JOYCE, Gerald F.
; TITLE OF INVENTION: NOVEL CATALYTIC RNA MOLECULES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 6063566th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,423
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/242,402
; FILING DATE: 13-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/270,180
; FILING DATE: 01-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April C.
; REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: TSRI 412.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
 JS-08-682-423-6

Query Match 1.1%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1047 TTTATGTTATTTATT 1061
 b 1 TTTATTTATTTATT 15

RESULT 145

JS-08-682-423-21/c
 Sequence 21, Application US/08682423
 Patent No. 6063566

GENERAL INFORMATION:
 APPLICANT: Joyce, Gerald F.
 TITLE OF INVENTION: NOVEL CATALYTIC RNA MOLECULES
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of
 ADDRESSEE: Patent Counsel
 STREET: 10666 No. 6063566th Torrey Pines Road, TPC-8
 CITY: La Jolla
 STATE: California
 COUNTRY: USA
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/682,423
 FILING DATE: 17-JUL-1996
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/242,402
 FILING DATE: 13-MAY-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/270,180
 FILING DATE: 01-JUL-1994
 ATTORNEY/AGENT INFORMATION:

NAME: Logan, April C.
 REGISTRATION NUMBER: 33,950
 REFERENCE/DOCKET NUMBER: TSRI 412.2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-554-2937
 TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
 JS-08-682-423-21

Query Match 1.1%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1047 TTTATGTTATTTATT 1061
 b 15 TTTATTTATTTATT 1

RESULT 146

S-09-167-151-13/c
 Sequence 13, Application US/09167151
 Patent No. 6307038
 GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: NOVEL ENZYMIC RNA MOLECULES

NUMBER OF SEQUENCES: 29

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

APPLICANT: TAKAHASHI, Tohru
 SERIZAWA, No. 6307038ufusa
 KOISHI, Ryuta
 KAWASHIMA, Ichiro
 TITLE OF INVENTION: EXPRESSION SYSTEMS UTILIZING
 AND A NOVEL REDUCING POLYPEPTIDE
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Friebsauf, Holtz, Goodman, Langer & Chick, P.C.
 STREET: 767 Third Avenue-25th Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10017-2023

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.24
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/167,151
 FILING DATE: 06-Oct-1998
 CLASSIFICATION: <Unknown>
 13-SEP-1994
 07-DEC-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/500,635
 FILING DATE: <Unknown>
 APPLICATION NUMBER: JP 6-218392
 FILING DATE: 13-SEP-1994
 APPLICATION NUMBER: JP 6-303809
 FILING DATE: 07-DEC-1994

ATTORNEY/AGENT INFORMATION:
 NAME: Goodman, Herbert
 REGISTRATION NUMBER: 17081
 REFERENCE/DOCKET NUMBER: 950376/HG
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 319-4900
 TELEFAX: (212) 319-5101
 TELEX: 236268

INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid, synthetic DNA
 HYPOTHETICAL: N
 ANTI-SENSE: N
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 US-09-167-151-13

Query Match 1.1%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1044 TTTATTTATTTATTTA 1058
 b 15 TTTATTTATTTATTTA 1

RESULT 147
 PCT-US95-05141-6
 Sequence 6, Application PC/TUS9505141
 GENERAL INFORMATION:

APPLICANT:
 TITLE OF INVENTION: NOVEL ENZYMIC RNA MOLECULES
 NUMBER OF SEQUENCES: 29
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05141
FILING DATE: 26-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,402
FILING DATE: 13-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,180
FILING DATE: 01-JUL-1994
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-05141-6

Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2Y 1047 TTTATGTTATTT 1061
|||||
Db 1 TTTATTTATTT 15

RESULT 148
PCT-US95-05141-21/c
Sequence 21, Application PC/TUS9505141
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: NOVEL ENZYMATIC RNA MOLECULES
NUMBER OF SEQUENCES: 29
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05141
FILING DATE: 26-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,402
FILING DATE: 13-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,180
FILING DATE: 01-JUL-1994
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-05141-21

Query Match 1.1%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1047 TTTATGTTATTT 1061
|||||
Db 15 TTTATTTATTT 1

RESULT 149
US-08-242-402-7
Sequence 7, Application US/08242402
Patent No. 5580967
GENERAL INFORMATION:
APPLICANT: JOYCE, GERALD F

TITLE OF INVENTION: OPTIMIZED CATALYTIC DNA-CLEAVING
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE, OFFICE OF
ADDRESS: PATENT COUNSEL
STREET: 10666 NORTH TORREY PINES ROAD, TPC 8
CITY: LA JOLLA
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,402
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LOGAN, APRIL C
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: TSRI 412.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-242-402-7

Query Match 1.1%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1047 TTTATGTTATTT 1061
|||||
Db 1 TTTATTTATTT 15

RESULT 150
US-08-242-402-12/c
Sequence 12, Application US/08242402
Patent No. 5580967
GENERAL INFORMATION:
APPLICANT: JOYCE, GERALD F
TITLE OF INVENTION: OPTIMIZED CATALYTIC DNA-CLEAVING
TITLE OF INVENTION: RIBOZYMES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE, OFFICE OF
ADDRESS: PATENT COUNSEL
STREET: 10666 NORTH TORREY PINES ROAD, TPC 8
CITY: LA JOLLA
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,402
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LOGAN, APRIL C

REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: TSRI 412.0
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
S-08-242-402-12

Query Match 1.1%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1047 TTTATGTTATTT 1061
15 TTTATTTATTT 1

RESULT 151
3-08-682-423-22
Sequence 22, Application US/08682423
Patent No. 6063566
GENERAL INFORMATION:
APPLICANT: Joyce, Gerald F.
TITLE OF INVENTION: NOVEL CATALYTIC RNA MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 6063566th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,423
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,402
FILING DATE: 13-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,180
FILING DATE: 01-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: TSRI 412.2
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
S-08-682-423-22

Query Match 1.1%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1047 TTTATGTTATTT 1061
DB 1 TTTATTTATTT 15

RESULT 152
US-08-682-423-25/c
Sequence 25, Application US/08682423
Patent No. 6063566
GENERAL INFORMATION:
APPLICANT: Joyce, Gerald F.
TITLE OF INVENTION: NOVEL CATALYTIC RNA MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 6063566th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,423
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,402
FILING DATE: 13-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,180
FILING DATE: 01-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: TSRI 412.2
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-682-423-25

Query Match 1.1%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1047 TTTATGTTATTT 1061
DB 15 TTTATTTATTT 1

RESULT 153
PCT-US95-05141-22
Sequence 22, Application PC/TUS9505141
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: NOVEL ENZYMATIC RNA MOLECULES
NUMBER OF SEQUENCES: 29
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05141
FILING DATE: 26-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,402
FILING DATE: 13-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,180
FILING DATE: 01-JUL-1994
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
CT-US95-05141-22

Query Match 1.1%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1047 TTTATGTATTATT 1061
b 1 TTTATTATTATT 15

RESULT 154
CT-US95-05141-25/c
Sequence 25, Application PC/TUS9505141
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: NOVEL ENZYMATIC RNA MOLECULES
NUMBER OF SEQUENCES: 29
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05141
FILING DATE: 26-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,402
FILING DATE: 13-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,180
FILING DATE: 01-JUL-1994
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
CT-US95-05141-25

Query Match 1.1%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1047 TTTATGTATTATT 1061
b 15 TTTATTATTATT 1

RESULT 155
S-08-281-940-54/c
Sequence 54, Application US/08281940
Patent No. 5589330
GENERAL INFORMATION:
APPLICANT: SHUBER, ANTHONY P.

TITLE OF INVENTION: METHOD FOR MULTIPLE ALLELE-SPECIFIC
TITLE OF INVENTION: DISEASE ANALYSIS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY P.C.
STREET: 805 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,940
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LUDWIG, S. PETER
REGISTRATION NUMBER: 25351
REFERENCE/DOCKET NUMBER: 0372/09696
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/527-7700
TELEFAX: 212/753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: Homo sapien
IMMEDIATE SOURCE:
CLONE: 21843AN
US-08-281-940-54

Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1207 AACCAACACACAAAT 1221
Db 16 AACCAACACACAAAT 2

RESULT 156
US-08-373-124A-970/c
Sequence 970, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZIMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 970:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-970

Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1617 AAATATATAATTGTT 1631
|||||
16 AAATATATAATTTT 2

RESULT 157
US-08-373-124A-2051/C
Sequence 2051, Application US/08/373,124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2051:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-2051

Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1617 AAATATATAATTGTT 1631
|||||
16 AAATATATAATTTT 2

RESULT 158
US-08-435-628-970/C
Sequence 970, Application US/08/435,628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 970:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-970

Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1617 AAAATATAATTGTT 1631
|||||
DB 16 AAAATATAATTTT 2

RESULT 159
US-08-435-628-2051/c
; Sequence 2051, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2051:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-2051

Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1617 AAAATATAATTGTT 1631
|||||
DB 16 AAAATATAATTTT 2

RESULT 160
US-08-710-134-54/c
; Sequence 54, Application US/08710134
; Patent No. 5834181
; GENERAL INFORMATION:
; APPLICANT: SHUBER, ANTHONY P.
; TITLE OF INVENTION: HIGH THROUGHPUT SCREENING METHOD FOR
; TITLE OF INVENTION: SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genzyme Corporation
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,134
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-8.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotides"
US-08-710-134-54

Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1207 AAACAAACAAACAT 1221
|||||
DB 16 AAACAAACAAACAT 2

RESULT 161
US-08-485-885-54/c
; Sequence 54, Application US/08485885

```

Patent No. 5849483
GENERAL INFORMATION:
APPLICANT: SHUBER, ANTHONY P.
TITLE OF INVENTION: HIGH THROUGHPUT SCREENING METHOD FOR
SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genzyme Corporation
STREET: One Mountain Road
CITY: Framingham
STATE: Massachusetts
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,895
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: GEN4-12.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotides"
S-08-485-895-54

Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1207 AAACAACAAACAACT 1221
b 16 AAACAACAAACAACT 2

RESULT 162
S-08-584-040-2299/c
Sequence 2299, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:

```

```

MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2299:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-2299

Query Match 1.1%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 749 TAGAATGTGATTT 763
Db 17 TAGAATGTGACATTT 3

RESULT 163
US-08-584-040-2785
Sequence 2785, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:

```



```

; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2785:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; JS-08-584-040-2785
;
; Query Match 1.1%; Score 13.4; DB 1; Length 17;
; Best Local Similarity 60.0%; Pred. No. 1.6e+02;
; Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
;
; 2Y 803 ATAAAGTCAATTGA 817
; Db 2 AUAACUCAAUUA 16
;
; RESULT 164
; JS-08-584-040-7818/c
; Sequence 7818, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lyon & Lyon
; STREET: 533 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7818:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
;
; US-08-584-040-7818
;
; Query Match 1.1%; Score 13.4; DB 1; Length 17;
; Best Local Similarity 93.3%; Pred. No. 1.6e+02;
; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 616 ACAAAAACACAAA 630
; Db 15 ACAAAAACACAAA 1
;
; RESULT 165
; US-09-371-772B-844/c
; Sequence 844, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 844
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
;
; US-09-371-772B-844
;
; Query Match 1.1%; Score 13.4; DB 1; Length 17;
; Best Local Similarity 93.3%; Pred. No. 1.6e+02;
; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 749 TAGAATGTGATTTT 763
; Db 17 TAGAATGTGATTTT 3
;
; RESULT 166
; US-09-371-772B-1309
; Sequence 1309, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1309
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

```



```
RESULT 171
US-09-316-083-22
; Sequence 22, Application US/09316083A
; Patent No. 6280942
; GENERAL INFORMATION:
; APPLICANT: The Institute of Physical and Chemical Research
; TITLE OF INVENTION: Endonuclease
; FILE REFERENCE: PH-651
; CURRENT APPLICATION NUMBER: US/09/316.083A
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: JP98/141861
; EARLIER FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
JS-09-316-083-22
Query Match 1.1%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred.No.1.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2y 1282 ATTATTGTTTATCTG 1296
||||| ||||| |||||
db 3 ATTATTGTTTATCTG 17

RESULT 172
JS-09-933-700-22
; Sequence 22, Application US/09933700
; Patent No. 6528296
; GENERAL INFORMATION:
; APPLICANT: The Institute of Physical and Chemical Research
; TITLE OF INVENTION: Endonuclease
; FILE REFERENCE: PH-651
; CURRENT APPLICATION NUMBER: US/09/933.700
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 09/316.083
; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
JS-09-933-700-22
Query Match 1.1%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred.No.1.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2y 1282 ATTATTGTTTATCTG 1296
||||| ||||| |||||
db 3 ATTATTGTTTATCTG 17

RESULT 173
JS-08-222-177A-345/c
; Sequence 345, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (GC-CA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DeWitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222.177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 345:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfg108p2
US-08-222-177A-345
Query Match 1.1%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred.No.2.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 957 AGTCATGTTGTGAGG 971
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Db 17 AGTCATGTTGTGAGG 3

RESULT 174
US-08-468-551-8
; Sequence 8, Application US/08468551
; Patent No. 5874212
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Rock, Matthew J.
; APPLICANT: Ganguly, Arupa
; TITLE OF INVENTION: DETECTION OF SINGLE BASE MUTATIONS AND
; TITLE OF INVENTION: OTHER VARIATIONS IN DOUBLE STRANDED DNA BY
; TITLE OF INVENTION: CONFORMATION-SENSITIVE CELL ELECTROPHORESIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
; STREET: FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/468,551
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Doyle Leary Ph.D., Kathryn
 REGISTRATION NUMBER: 36,317
 REFERENCE/DOCKET NUMBER: 9855-501
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-965-1284
 TELEFAX: 215-567-2991
 TELEX: 831-494

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

S-08-468-551-8

Query Match 1.1%; Score 13.4; DB 1; Length 19;

Best Local Similarity 93.3%; Pred. No. 2.1e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 818 GCTGGAATCCTGGA 832

|||||

C 1 GCTGGAATCCTGGA 15

RESULT 175

S-09-422-978-4969

Sequence 4969, Application US/09422978

Patent No. 6537751

GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta

APPLICANT: Cohen, Daniel

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET 020CPI

CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT FILING DATE: 1999-10-20

EARLIER APPLICATION NUMBER: US 09/298,850

EARLIER FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER FILING DATE: 1998-11-23

EARLIER APPLICATION NUMBER: US 60/082,614

EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 4969

LENGTH: 19

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: primer_bind

LOCATION: 1..19

OTHER INFORMATION: upstream amplification primer 99-1944 for SEQ 1035,

S-09-422-978-4969

Query Match

Best Local Similarity 1.1%; Score 13.4; DB 1; Length 19;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1567 TTTTACTGTTTCTGAT 1581

|||||

C 1 TTTTACTGTTTCTGAT 15

RESULT 176

S-08-271-942A-92/c

Sequence 92, Application US/08271942A

Patent No. 5550020

GENERAL INFORMATION:

APPLICANT: Gallie, Brenda L.

APPLICANT: Dunn, James M.
 APPLICANT: Stevens, John K.
 TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
 and Targeted Screening for Retinoblastoma
 NUMBER OF SEQUENCES: 123
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Oppedahl & Larson
 STREET: 1992 Commerce Street, Suite 309
 CITY: Yorktown Heights
 STATE: NY
 COUNTRY: USA
 ZIP: 10598-4412
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS 5.0
 SOFTWARE: Word Perfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/271,942A
 FILING DATE: 08-JUL-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Marina T. Larson
 REGISTRATION NUMBER: 32,038
 REFERENCE/DOCKET NUMBER: VGEN.P-003-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 245-3252
 TELEFAX: (914) 962-4330
 TELEX:
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 HYPOTHETICAL: no
 ANTI-SENSE: no
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: human
 FEATURE:
 NAME/KEY: primer for exon 11 of human RBI gene
 US-08-271-942A-92

Query Match

Best Local Similarity 1.1%; Score 13.2; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1566 TTTTACTGTTTCTGATT 1583

|||||

Db 18 TTTATAGTTCAGATT 1

RESULT 177

US-08-779-916A-92/c

Sequence 92, Application US/08779916A

Patent No. 6063567

GENERAL INFORMATION:

APPLICANT: Gallie, Brenda L.

APPLICANT: Dunn, James M.

APPLICANT: Stevens, John K.

APPLICANT: Hui, May

TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis

and Targeted Screening for Retinoblastoma

NUMBER OF SEQUENCES: 123

CORRESPONDENCE ADDRESS:

ADDRESSEE: Oppedahl & Larson

STREET: 1992 Commerce Street, Suite 309

CITY: Yorktown Heights

STATE: NY
COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,916A
FILING DATE: 07-JAN-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/271,942
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-003-US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: human
FEATURES:
NAME/KEY: primer for exon 11 of human Rb1 gene
US-08-779-916A-92

Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1566 TTTTACTGTTTCGATT 1583
DB 18 TTATAGTGTTCAGATT 1

RESULT 178
US-09-474-922A-81/c
Sequence 81, Application US/09474922A
Patent No. 6187586
GENERAL INFORMATION:
APPLICANT: Brett P. Monla
APPLICANT: Lex M. Cowsett
APPLICANT: Richard A. Roth
TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
FILE REFERENCE: RTS-0036
CURRENT APPLICATION NUMBER: US/09/474,922A
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 81
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-474-922A-81

Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1596 AAAAGTAATATGAACA 1613
DB 18 AAAGAAATATGAGACA 1
RESULT 179
US-09-637-751A-6/c
Sequence 6, Application US/09637751A
Patent No. 6383754
GENERAL INFORMATION:
APPLICANT: Kaufman, Joseph C.
APPLICANT: Roth, Matthew E.
APPLICANT: Lizardi, Paul M.
APPLICANT: Feng, Li
APPLICANT: Latimer, Darin R.
TITLE OF INVENTION: Binary Encoded Sequence Tags
Patent No. 6383754
FILE REFERENCE: AGL 100
CURRENT APPLICATION NUMBER: US/09/637,751A
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-637-751A-6

Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 616 ACACAAACACACAAATTA 633
DB 18 ACACAAACAAACAAATTA 1

RESULT 180
US-09-144-367-15
Sequence 15, Application US/09144367
Patent No. 6432639
GENERAL INFORMATION:
APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/09/144,367
CURRENT FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/058,612
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 18
TYPE: DNA
ORGANISM: H. sapiens
US-09-144-367-15

Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 414 CAGAATCAGTGAAGATG 431
DB 1 CAAGAAACAGAGAAGAG 18

RESULT 181
US-09-144-367-29
Sequence 29, Application US/09144367
Patent No. 6432639

GENERAL INFORMATION:
APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/09/144,367
CURRENT FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/058,612
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 18
TYPE: DNA
ORGANISM: H. sapiens
S-09-144-367-29

Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

414 CAAGATCAGTGAAGATG 431
1 CAAGAACAAGAGAGAGG 18

RESULT 182
S-09-475-947A-260
Sequence 260, Application US/09475947A
Patent No. 6472154

GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: DTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 260
LENGTH: 18
TYPE: DNA
ORGANISM: human
S-09-475-947A-260

Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

819 CTGGAATCTCGATTTT 836
1 CTGGAAGACATGGATTTT 18

RESULT 183
S-09-422-978-5436/C
Sequence 5436, Application US/09422978
Patent No. 6537751

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPL
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 5436
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/Key: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-25716 for SEQ 1502,
US-09-422-978-5436

Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

421 CAGTGAAGATGCCAGTGA 438
18 CAGTGAAGGTGCAGTTA 1

RESULT 184
US-09-068-506-71
Sequence 71, Application US/09068506A
Patent No. 6569618
GENERAL INFORMATION:
APPLICANT: YASUE, Hirofumi
APPLICANT: YOSHIMURA, Kumamoto
TITLE OF INVENTION: DIAGNOSIS OF DISEASES ASSOCIATED WITH CORONARY
FILE REFERENCE: 0032-245P
CURRENT APPLICATION NUMBER: US/09/068,506A
CURRENT FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 71
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primers
US-09-068-506-71

Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1355 GTGTTGCTAGTCTCTGCT 1372
1 GGGTTTGTAGTCTGCTGT 18

RESULT 185
PCT-US95-08604-92/c
Sequence 92, Application PC/TUS9508604
GENERAL INFORMATION:
APPLICANT: Visible Genetics Inc.
APPLICANT: HSC Research and Development Limited Partnership
APPLICANT: Gallie, Brenda L.
APPLICANT: Dunn, James M.
APPLICANT: Stevens, John K.
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
NUMBER OF INVENTION: and Targeted Screening for Retinoblastoma
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESS: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
STATE: NY
COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08604
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,942
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-003-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: human
FEATURE:
NAME/KEY: primer for exon 11 of human RBL gene
PCT-US95-08604-92

Query Match 1.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1566 TTTTACTGTTTCTGATT 1583
DB 18 TTATAGTGTTCAGATT 1

RESULT 186
US-08-435-605A-48/c
Sequence 48, Application US/08435605A
Patent No. 5874287
GENERAL INFORMATION:
APPLICANT: Burnette, W. Neal
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,605A
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: A-1969

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
US-08-435-605A-48

Query Match 1.0%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1412 AAAACTCCACAGT 1424
DB 13 AAAACTCCACAGT 1

RESULT 187
US-08-882-649A-9/c
Sequence 9, Application US/08882649A
Patent No. 6344316
GENERAL INFORMATION:
APPLICANT: Lockhart, David J.
Chee, Mark
Gunderson, Kevin
Chaoqiang, Lai
Wodicka, Lisa
Cronin, Maureen T.
Lee, Danny
Tran, Huu M.
Matsuzaki, Hajime
McGall, Glenn H.
TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joe Liebeschuetz
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,649A
FILING DATE: 25-Jun-1997
CLASSIFICATION: 435-006.000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010,471
FILING DATE: 23-JAN-1996
APPLICATION NUMBER: US 60/035,170
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: PCT/US97/01603
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-019410US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: YES
 SEQUENCE DESCRIPTION: (ix) Features:
 SEQUENCE DESCRIPTION: SEQ ID NO: 9:

S-08-882-649A-9

Query Match 1.0%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1143 TTTATTTATTTT 1155
 13 TTTATTTATTTT 1

RESULT 188
 S-08-334-847-510/c
 Sequence 510, Application US/08334847
 Patent No. 5693532

GENERAL INFORMATION:
 APPLICANT: McSwiggen, James
 APPLICANT: Draper, Kenneth
 APPLICANT: Pavco, Pam
 APPLICANT: Woolf, Tod
 TITLE OF INVENTION: METHOD AND REAGENT FOR
 TITLE OF INVENTION: INHIBITING RESPIRATORY
 TITLE OF INVENTION: SYNCYTIAL VIRUS
 NUMBER OF SEQUENCES: 909
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/334.847
 FILING DATE: No. 5693532ember 4, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 209/032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 510:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

S-08-334-847-510

Query Match 1.0%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

525 ATTGAATTTCAG 537
 13 ATTGAATTTCAG 1

SULT 189

US-08-311-486C-188
 Sequence 188, Application US/08311486C
 Patent No. 5811300

GENERAL INFORMATION:
 APPLICANT: Sean Sullivan
 APPLICANT: Kenneth Draper
 APPLICANT: Kevin Kisch
 APPLICANT: Dan T. Stinchcomb
 APPLICANT: James McSwiggen
 TITLE OF INVENTION: RIBOZYME TREATMENT OF
 TITLE OF INVENTION: DISEASES OR CONDITIONS
 TITLE OF INVENTION: RELATED TO LEVELS OF
 TITLE OF INVENTION: TNF-
 NUMBER OF SEQUENCES: 1157
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/311.486C
 FILING DATE: September 23, 1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA: described below:
 APPLICATION NUMBER: 08/008.895
 FILING DATE: January 19, 1993
 APPLICATION NUMBER: 07/989.849
 FILING DATE: December 7, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 209/166
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 188:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-311-486C-188

Query Match 1.0%; Score 13; DB 1; Length 15;
 Best Local Similarity 30.8%; Pred. No. 1.4e+02;
 Matches 4; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1038 TATTATTATTTA 1050
 DB 3 UAUUUUAUUUA 15

RESULT 190

US-08-311-486C-196
 Sequence 196, Application US/08311486C
 Patent No. 5811300

GENERAL INFORMATION:
 APPLICANT: Sean Sullivan
 APPLICANT: Kenneth Draper
 APPLICANT: Kevin Kisch
 APPLICANT: Dan T. Stinchcomb

APPLICANT: Sean Sullivan
 APPLICANT: Kenneth Draper
 APPLICANT: Kevin Kisch
 APPLICANT: Dan T. Stinchcomb
 APPLICANT: James McGaughen
 TITLE OF INVENTION: RIBOSYME TREATMENT OF
 TITLE OF INVENTION: DISEASES OR CONDITIONS
 TITLE OF INVENTION: RELATED TO LEVELS OF
 TITLE OF INVENTION: TW-
 NUMBER OF SEQUENCES: 1157
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon

APPLICANT: Kenneth Draper
APPLICANT: Kevin Kisich
APPLICANT: Dan T. Stanchcomb
APPLICANT: James McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITION
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF-
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb

MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,486C
FILING DATE: September 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including app
PRIOR APPLICATION DATA: described be
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warbur, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 720:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-311-486C-720

Query Match 1.0%; Score 13; DB 1; Length 15;
Best Local Similarity 30.8%;
Pred. No. 1.4e+02;
Matches 4; Conservative 9; Mismatches 0; Indels

Y 1038 TATTATTATTA 1050
3 UAUUUUUUUU 15

ESULT 193
S-07-977-284A-168/c
Sequence 168, Application US/07977284A
Patent No. 5558988

GENERAL INFORMATION:
APPLICANT: PROCKOP, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Williams, Charlene J.
APPLICANT: Ritvanenmi, Pertti
APPLICANT: Baldwin, Clinton
APPLICANT: Hopkinson, Ian
APPLICANT: Ahmad, Nilofar Nina
TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 55589898iris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,284A
FILING DATE: 13-NOV-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

/ FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: DeLuca, Mark
 / REGISTRATION NUMBER: 33,229
 / REFERENCE/DOCKET NUMBER: TUL-0697
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (215) 568-3100
 / TELEFAX: (215) 568-3439
 / INFORMATION FOR SEQ ID NO: 168:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 17
 / TYPE: NUCLEIC ACID
 / STRANDEDNESS: SINGLE
 / TOPOLOGY: LINEAR
 / ANTI-SENSE: NO
 / US-07-977-284A-168

```

Query Match      1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      744  TTTGCTAGAAATCT 756
          |||||
Db       15  TTTGCTAGAAATCT 3

```

RESULT 194
 US-08-249-037C-17
 Sequence 17, Application US/08249037C
 Patent No. 5928917
 GENERAL INFORMATION:
 APPLICANT: Kilburn, Douglas G.
 APPLICANT: Miller, Robert C.
 APPLICANT: Warren, Richard A.J.
 APPLICANT: Gilkes, Neil R.
 TITLE OF INVENTION: Polysaccharide binding fusion proteins
 and conjugates
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rae-Venter Law Group, P.C.
 STREET: P.O.Box 50039
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/249,037C
 FILING DATE: 24-MAY-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/865,095
 FILING DATE: 08-APR-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/603,987
 FILING DATE: 25-OCT-1990
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/216,794
 FILING DATE: 08-JUL-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Kung, Viola T.
 REGISTRATION NUMBER: 41,131
 REFERENCE/DOCKET NUMBER: CBDT.002.04US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)328-4400
 TELEFAX: (650)328-4477
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs

schultz143-3.rni

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-249-037C-17

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1084 AATTGGGAAAAAT 1096
b 1 AATTGGGAAAAAT 13

RESULT 195

US-08-256-426B-168/c
Sequence 168, Application US/08256426B
Patent No. 5948611
GENERAL INFORMATION:
APPLICANT: Prockop, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Williams, Charlene J.
APPLICANT: Ritvanemi, Pertti
APPLICANT: Baldwin, Clinton
APPLICANT: Hopkinson, Ian
APPLICANT: Ahmad, Nilofar Nina
TITLE OF INVENTION: Methods of Detecting A Genetic
NUMBER OF SEQUENCES: 293
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,426B
FILING DATE: 03-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10964
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,284
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mark Deluca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TTU-1082
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACTERISTICS:
LENGTH: 17
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
ANTI-SENSE: NO
US-08-256-426B-168

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 TTGCTAGATGT 756
|||||

Db 15 TTGCTAGATGT 3

RESULT 196

US-08-788-622B-17
Sequence 17, Application US/08788622B
Patent No. 5962289
GENERAL INFORMATION:
APPLICANT: Kilburn, Douglas G.
APPLICANT: Miller, Robert C.
APPLICANT: Warren, Richard A.J.
APPLICANT: Gilkes, Neil R.
TITLE OF INVENTION: Polysaccharide binding fusion proteins
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rae-Venter Law Group, P.C.
STREET: P.O.Box 60039
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,622B
FILING DATE: January 23, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,037
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,095
FILING DATE: 08-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,987
FILING DATE: 25-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/216,794
FILING DATE: 08-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: KUDS, Viola T.
REGISTRATION NUMBER: 41,131
REFERENCE/DOCKET NUMBER: CHDT.002.06US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
TELEFAX: (650)328-4477
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-788-622B-17

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AATTGGGAAAAAT 1096
b 1 AATTGGGAAAAAT 13

RESULT 197

US-08-985-162-514
Sequence 514, Application US/08985162
Patent No. 6057156
GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir

```

APPLICANT: Pell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 514:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
3-08-985-162-514

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 38.5%; Pred. No. 2e+02;
Matches 5; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

550 AGTTTTCATTGT 562
||||:||||:|
5 AGUUUUCAUGU 17

RESULT 198
3-08-985-162-515
Sequence 515, Application US/08985162
Patent No. 6057156
GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Pell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

```

```

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 515:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-985-162-515

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 38.5%; Pred. No. 2e+02;
Matches 5; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

550 AGTTTTCATTGT 562
||||:||||:|
4 AGUUUUCAUGU 16

RESULT 199
US-08-985-162-516
Sequence 516, Application US/08985162
Patent No. 6057156
GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Pell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997

```

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 516:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
JS-08-985-162-516

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 38.5%; Pred. No. 2e+02;
Matches 5; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 550 AGTTTTCATTGT 562
DB 3 AGUUUUCAUUGU 15

RESULT 200
JS-08-985-162-517
; Sequence 517, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Fast-Seq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 517:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-985-162-517

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 38.5%; Pred. No. 2e+02;
Matches 5; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 550 AGTTTTCATTGT 562
DB 2 AGUUUUCAUUGU 14

RESULT 201
US-08-788-621B-17
; Sequence 17, Application US/08788621B
; Patent No. 6124117
; GENERAL INFORMATION:
; APPLICANT: Kilburn, Douglas G.
; APPLICANT: Miller, Robert C.
; APPLICANT: Warren, Richard A.J.
; APPLICANT: Gilkes, Neil R.
; TITLE OF INVENTION: Polysaccharide binding fusion proteins
; TITLE OF INVENTION: and conjugates
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rae-Venter Law Group, P.C.
; STREET: P.O.Box 60039
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,621B
; FILING DATE: January 23, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/249,037
; FILING DATE: 24-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865,095
; FILING DATE: 08-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,987
; FILING DATE: 25-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/216,794
; FILING DATE: 08-JUL-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Kung, Viola T.
; REGISTRATION NUMBER: 41,131
; REFERENCE/DOCKET NUMBER: CBOT.002.05US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)328-4400
; TELEFAX: (650)328-4477
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-788-621B-17

Query Match 1.0%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AATTTGGAAAT 1096
DB 1 AATTTGGAAAT 13

```

RESULT 202
3-09-067-773-28/c
Sequence 28, Application US/09067773
Patent No. 5976805
GENERAL INFORMATION:
APPLICANT: You, Qimin
TITLE OF INVENTION: A Neisseria gonorrhoeae specific DNA
TITLE OF INVENTION: Fragment -- GC3
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Becton Dickinson and Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey
COUNTRY: USA
ZIP: 07417-6800
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,773
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hight, David W.
REFERENCE/DOCKET NUMBER: P-4088
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-847-6800
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
3-09-067-773-28

Query Match 1.0%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

756 TGATATTTGACGATC 771
|||||
16 TGACATTTGACGATC 1

RESULT 203
3-08-373-124A-974/c
Sequence 974, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:

```

```

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 974:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-974

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1613 ATTAAATATATAATTT 1628
DB 17 AATAAAATATAATTT 2

RESULT 204
US-08-373-124A-2037
Sequence 2037, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:

```

FALOR REFLECTION DATA: 08/245,455
 APPLICATION NUMBER: 08/192,943
 FILING DATE: May 18, 1994
 APPLICATION NUMBER: 08/192,943
 FILING DATE: February 7, 1994
 APPLICATION NUMBER: 07/987,132
 FILING DATE: December 7, 1992
 APPLICATION NUMBER: 07/936,422
 FILING DATE: August 26, 1992
 ATTORNEY/AGENT INFORMATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/0351
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2153:
SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
5-08-373-124A-2153

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 18.8%; Pred. No. 2.3e+02;
Matches 3; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

1 1040 TTATATTTATGAT 1055
2 UUUUUUUUUUAU 17

RESULT 207

3-08-373-124A-2155
Sequence 2155, Application US/08373124A
Patent No. 5646042

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2155:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

1-08-373-124A-2155

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 18.8%; Pred. No. 2.3e+02;
Matches 3; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 1040 TTATATTTATGAT 1055
DB 1 UUUUUUUUUUAU 16

RESULT 208

US-08-435-628-974/C
Sequence 974, Application US/08435628
Patent No. 5817796

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 974:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-435-628-974

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1613 ATTTAAATATAATTT 1628
DB 17 AATAAATATAATTT 2

LT 210
B-435-628-2055/c
quence 2055, Application US/08435628
cent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McGswigen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: TREATMENT
TITLE OF INVENTION: CANCER US

```

STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2155:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-2155

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 18.8%; Prd. No. 2.3e+02;
Matches 3; Conservative 1; Mismatches 2; Indels

QY 1040 TTTATTATTATGAT 1055
Db 1 UUUUUUUUUUUUU 16
::|:: ::|::|::

RESULT 213
US-08-527-060-23/c
Sequence 23, Application US/08527060
Patent No. 5834440
GENERAL INFORMATION:
APPLICANT: Goldenberg, Tsvi
APPLICANT: Tritz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT
TITLE OF INVENTION: AND/OR PREVENTION OF RESTENOSIS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/527,060

```

FILING DATE: 12-SEP-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: McWaters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480124.402C1
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
S-08-527-060-23

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1172 TTTATTAGATAAATTT 1187
b 16 TTTATTAGATAAATTT 1

RESULT 214
S-08-292-620A-1983
Sequence 1983, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McWissen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

two

TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1983:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1983

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 31.2%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1047 TTTATGTATTATTATTA 1062
DB 2 UUGAUGUAUUUAUAA 17

RESULT 215
US-09-067-773-29/c
Sequence 29, Application US/09067773
Patent No. 5976805
GENERAL INFORMATION:
APPLICANT: You, Qimin
TITLE OF INVENTION: A Neisseria gonorrhoeae Specific DNA
TITLE OF INVENTION: Fragment -- GC3
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Becton Dickinson and Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: New Jersey
COUNTRY: USA
ZIP: 07417-6800
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,773
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hightet, David W.
REFERENCE/DOCKET NUMBER: P-4088
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-847-6800
TELEFAX: 201-848-9228
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-09-067-773-29

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 756 TGATATTGAGCATC 771
DB 17 TGATATTGAGCATC 2

RESULT 216
US-08-988-706-17/c
Sequence 17, Application US/08988706
Patent No. 6083698
GENERAL INFORMATION:

APPLICANT: OLSEN, Sheri J.
APPLICANT: ANGELLY, Tracy S.
APPLICANT: LAWRENCE, Tammy
APPLICANT: LESCALLETT, Jennifer L.
APPLICANT: MURPHY, Patricia D.
APPLICANT: ALLEN, Antonette P.
APPLICANT: THRUBER, Denise B.
APPLICANT: WHITE, Marga B.
APPLICANT: ZENG, Bin
APPLICANT: SADZEWICZ, Lisa K.
TITLE OF INVENTION: CANCER SUSCEPTIBILITY MUTATIONS OF BRCA1
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: OncorMed, Inc.
STREET: 205 Perry Parkway
CITY: Gaithersburg
STATE: MD
COUNTRY: USA
ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,706
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: TARCZA, John E.
REGISTRATION NUMBER: 33,638
REFERENCE/DOCKET NUMBER: PA-0108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-208-1888
TELEFAX: 301-926-6125
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PROBE"
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
STRAIN: BRCA1
3-08-988-706-17

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
524 AATTGCAATTCAGTA 539
17 AATTGCAATTCAGTA 2

RESULT 217
3-08-988-706-18/c
Sequence 18, Application US/08988706
Patent No. 6083698
GENERAL INFORMATION:
APPLICANT: OLSEN, Sheri J.
APPLICANT: ANGELLY, Tracy S.
APPLICANT: LAWRENCE, Tammy
APPLICANT: LESCALLETT, Jennifer L.
APPLICANT: MURPHY, Patricia D.
APPLICANT: ALLEN, Antonette P.
APPLICANT: THRUBER, Denise B.
APPLICANT: WHITE, Marga B.

APPLICANT: ZENG, Bin
APPLICANT: SADZEWICZ, Lisa K.
TITLE OF INVENTION: CANCER SUSCEPTIBILITY MUTATIONS OF BRCA1
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: OncorMed, Inc.
STREET: 205 Perry Parkway
CITY: Gaithersburg
STATE: MD
COUNTRY: USA
ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,706
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: TARCZA, John E.
REGISTRATION NUMBER: 33,638
REFERENCE/DOCKET NUMBER: PA-0108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-208-1888
TELEFAX: 301-926-6125
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PROBE"
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
STRAIN: BRCA1
US-08-988-706-18

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
524 AATTGCAATTCAGTA 539
17 AATTGCAATTCAGTA 2

RESULT 218
US-09-071-845-1983
Sequence 1893, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles

APPLICANT: ZENG, Bin
APPLICANT: SADZEWICZ, Lisa K.
TITLE OF INVENTION: CANCER SUSCEPTIBILITY MUTATIONS OF BRCA1
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: OncorMed, Inc.
STREET: 205 Perry Parkway
CITY: Gaithersburg
STATE: MD
COUNTRY: USA
ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,706
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: TARCZA, John E.
REGISTRATION NUMBER: 33,638
REFERENCE/DOCKET NUMBER: PA-0108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-208-1888
TELEFAX: 301-926-6125
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PROBE"
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
STRAIN: BRCA1
US-08-988-706-18

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
524 AATTGCAATTCAGTA 539
17 AATTGCAATTCAGTA 2

RESULT 218
US-09-071-845-1983
Sequence 1893, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles

APPLICANT: ZENG, Bin
APPLICANT: SADZEWICZ, Lisa K.
TITLE OF INVENTION: CANCER SUSCEPTIBILITY MUTATIONS OF BRCA1
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: OncorMed, Inc.
STREET: 205 Perry Parkway
CITY: Gaithersburg
STATE: MD
COUNTRY: USA
ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,706
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: TARCZA, John E.
REGISTRATION NUMBER: 33,638
REFERENCE/DOCKET NUMBER: PA-0108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-208-1888
TELEFAX: 301-926-6125
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PROBE"
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
STRAIN: BRCA1
US-08-988-706-18

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
524 AATTGCAATTCAGTA 539
17 AATTGCAATTCAGTA 2

RESULT 218
US-09-071-845-1983
Sequence 1893, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles

```

STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1983:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1983

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```

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 31.2%; Pred. No. 2.3e+02;
Matches 5; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1047 TTTATGTATTATTTA 1062
DB 2 UUGAUGAUUUAUUA 17

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```

RESULT 219
US-08-584-040-2166/c
Sequence 2166, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
OPERATING SYSTEM: IBM P.C. DOS 5.0

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SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2166:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-2166

```

```

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1586 ATGGAATATATAAGT 1601
DB 16 ATGGAAGATTAAGT 1

```

```

RESULT 220
US-08-584-040-2556/c
Sequence 2556, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 2556:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

3-08-584-040-2556

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1085 ATTGGAAAAATAGAA 1100
|||||
D 17 ATTGGAAAAATAGAA 2

RESULT 221

3-08-584-040-2557/c
Sequence 2557, Application US/08584040
Patent No. 6346398

GENERAL INFORMATION:

APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/584,040

FILING DATE: January 11, 1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/005,974

FILING DATE: October 26, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 218/064

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 2557:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

3-08-584-040-2557

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1085 ATTGGAAAAATAGAA 1100
|||||
DB 16 ATTGGAAAAATAGAA 1

RESULT 222

US-08-584-040-2828/c

; Sequence 2828, Application US/08584040

; Patent No. 6346398

; GENERAL INFORMATION:

; APPLICANT: Pavco, Pamela

; APPLICANT: McSwiggen, James

; APPLICANT: Stinchcomb, Dan T.

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: METHOD AND REAGENT FOR THE

; TITLE OF INVENTION: TREATMENT OF DISEASES OR

; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS

; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL

; TITLE OF INVENTION: GROWTH FACTOR

; NUMBER OF SEQUENCES: 8502

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/584,040

; FILING DATE: January 11, 1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/005,974

; FILING DATE: October 26, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 218/064

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 2828:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-584-040-2828

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1201 TAGGTAACAAACAA 1216
|||||
DB 16 TAGGTAACAAACAA 1

RESULT 223

US-08-584-040-3850

; Sequence 3850, Application US/08584040

```

Query Match      1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 56.2%;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```

Qy 1116 GAATAGTTATAAAGAT 1131
| | | : : : | | | :
Db 2 GGAUATUUUAAAGAU 17

APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISORDERS OR
CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502

TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
 TITLE OF INVENTION: GROWTH FACTOR
 NUMBER OF SEQUENCES: 8502
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4226:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
3-08-584-040-4226

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Y 1116 GAATAGTATATAAGAT 1131
| | | | | | | | | | | | | | | | | | |
D 1 GGAUUAUUAAGAUA 16

RESULT 226
S-09-306-420C-2
Sequence 2, Application US/09306420C
Patent No. 6555311
GENERAL INFORMATION:
APPLICANT: LOCARNINI, STEPHEN A
APPLICANT: BARTHOLOMEUSZ, ANGELINE I
APPLICANT: AYE, THEIN T
APPLICANT: DEMAN, ROBERT A
TITLE OF INVENTION: VIRAL VARIANTS AND METHODS FOR DETECTING SAME
FILE REFERENCE: 2551-28
CURRENT APPLICATION NUMBER: US/09/306,420C
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: PCT/AU97/00520
PRIOR FILING DATE: 1997-08-15
PRIOR APPLICATION NUMBER: P03519
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 17
TYPE: DNA
ORGANISM: Hepatitis B virus
S-09-306-420C-2

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1556 CTCGAAATTTTITTA 1571
| | | | | | | | | | | | | | | | | | |
b 2 CTCGAAATTTTITTA 17

RESULT 227
S-09-306-420C-4
Sequence 4, Application US/09306420C
Patent No. 6555311
GENERAL INFORMATION:

APPLICANT: LOCARNINI, STEPHEN A
APPLICANT: BARTHOLOMEUSZ, ANGELINE I
APPLICANT: AYE, THEIN T
APPLICANT: DEMAN, ROBERT A
TITLE OF INVENTION: VIRAL VARIANTS AND METHODS FOR DETECTING SAME
FILE REFERENCE: 2551-28
CURRENT APPLICATION NUMBER: US/09/306,420C
CURRENT FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: PCT/AU97/00520
PRIOR FILING DATE: 1997-08-15
PRIOR APPLICATION NUMBER: P03519
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 17
TYPE: DNA
ORGANISM: Hepatitis B virus
US-09-306-420C-4

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1556 CTCGAAATTTTITTA 1571
| | | | | | | | | | | | | | | | | | |
Db 2 CTCGAAATTTTITTA 17

RESULT 228
US-09-371-772B-711/c
; Sequence 711, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 711
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-711

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1586 ATCGAAATATAAAGT 1601
| | | | | | | | | | | | | | | | | | |
Db 16 ATCGAAATATAAAGT 1

RESULT 229
US-09-371-772B-1080/c
; Sequence 1080, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim


```

; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1080
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1080

Query Match      1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DY 1085 ATTGCAAAATAGAA 1100
|||||
DB 17 ATTGCAAAATAGAA 2

RESULT 230
US-09-371-772B-1081/c
; Sequence 1081, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1081
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1081

Query Match      1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DY 1085 ATTGCAAAATAGAA 1100
|||||
DB 16 ATTGCAAAATAGAA 1

RESULT 231
US-09-371-772B-1352/c
; Sequence 1352, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan

```

```

; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1352
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1352

Query Match      1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1201 TAGATTAACCAACAA 1216
|||||
DB 16 TAGTAAACCAACAA 1

RESULT 232
US-09-371-772B-1617
; Sequence 1617, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1617
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1617

Query Match      1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1457 GTTTATTATGTACAAA 1472
|:|:|:|:|:|
DB 2 GUCUAUAUAGUACAA 17

RESULT 233
US-09-371-772B-1992
; Sequence 1992, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

```

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/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MHEH00.876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B
/ CURRENT FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1992
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ US-09-371-772B-1992

Query Match          1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

/ 1116 GAATAGTTATTAAGAT 1131
/      |||::|||::|||:
/      2 GGAUAUUUAUAAGAUA 17

RESULT 234
3-09-371-772B-1993
Sequence 1993, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
/ APPLICANT: Ribozyne Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MHEH00.876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B
/ CURRENT FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1993
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ US-09-371-772B-1993

Query Match          1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

/ 1116 GAATAGTTATTAAGAT 1131
/      |||::|||::|||:
/      1 GGAUAUUUAUAAGAUA 16

RESULT 235
3-09-371-772B-4747
Sequence 4747, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
/ APPLICANT: Ribozyne Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MHEH00.876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B
/ CURRENT FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4747
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ US-09-371-772B-4747

```

```

/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MHEH00.876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B
/ CURRENT FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4747
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ US-09-371-772B-4747

Query Match          1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

/ 935 ATTAGCCACCATCTTA 950
/      |||::|||::|||:
/      2 AUTGGCCACCAUCUGA 17

RESULT 236
US-09-371-772B-5267/c
Sequence 5267, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
/ APPLICANT: Ribozyne Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MHEH00.876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B
/ CURRENT FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 5267
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ US-09-371-772B-5267

Query Match          1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

/ 1347 TGCCAGCTGTGTGGT 1362
/      |||::|||::|||:
/      16 TCCCACTGTGTGGT 1

RESULT 237
US-09-371-772B-6945/c
Sequence 6945, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
/ APPLICANT: Ribozyne Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

```

FILE REFERENCE: M86B00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6945
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-6945

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1438 TTCTGCTGGTGA 1453
||| ||||| |||||
Db 17 TTCTGCTGGTGA 2

RESULT 238
US-09-371-772B-6946/c
Sequence 6946, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Growth of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: M86B00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6946
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-6946

Query Match 1.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1438 TTCTGCTGGTGA 1453
||| ||||| |||||
Db 16 TTCTGCTGGTGA 1

RESULT 239
US-08-867-941-37/c
Sequence 37, Application US/08867941
Patent No. 5977337
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M
APPLICANT: Du, Run-Pan
APPLICANT: Wang, QuiJun
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/867,941
FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-867-941-37

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1233 TTAATTTTCATTCA 1248
||| ||||| |||||
Db 18 TTAATTTTCATTCA 3

RESULT 240
US-09-200-141-22/c
Sequence 22, Application US/09200141
Patent No. 5985663
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF Interleukin-15 EXPRESSION
FILE REFERENCE: RTS-0022
CURRENT APPLICATION NUMBER: US/09/200,141
CURRENT FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 22
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-200-141-22

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1339 CTTCATTCAGCAGCT 1354
||| ||||| |||||
Db 16 CTTCATTCAGCAGCT 1

RESULT 241
US-09-339-964-42/c
Sequence 42, Application US/09339964
Patent No. 6025198
GENERAL INFORMATION:

APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-2 EXPRESSION
FILE REFERENCE: RTS-0065
CURRENT APPLICATION NUMBER: US/09/339,964
CURRENT FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 42

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

-09-339-964-42

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

469 TGTATCTGTGGTCT 484

16 TGTCTGTGGTCT 1

RESULT 242

-09-156-807-47/c

Sequence 47, Application US/09156807

Patent No. 6030786

GENERAL INFORMATION:

APPLICANT: Cowsett, Lex M.

TITLE OF INVENTION: ANTISENSE MODULATION OF RhoC EXPRESSION

FILE REFERENCE: RTS-0014

CURRENT APPLICATION NUMBER: US/09/156,807

CURRENT FILING DATE: 1998-09-18

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 47

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

-09-156-807-47

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

827 CCTGAGTTTTTCTG 842

18 CCTGAGTTGTTCTG 3

SULT 243

-09-289-377-22/c

Sequence 22, Application US/09289377

Patent No. 6046321

GENERAL INFORMATION:

APPLICANT: Lex M. Cowsett

TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-11 EXPRESSION

FILE REFERENCE: RTS-0058

CURRENT APPLICATION NUMBER: US/09/289,377

CURRENT FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 22

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

-09-289-377-22

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1486 TATTATTAAATGACT 1501

Db 18 TACTATTGATGACT 3

RESULT 244

US-09-074-658-37/c

Sequence 37, Application US/09074658

Patent No. 6184371

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M

APPLICANT: Run-Pan Du

APPLICANT: Quijun Wang

APPLICANT: Yang, Yan-Ping

APPLICANT: Klein, Michel H

TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA

NUMBER OF SEQUENCES: 78

CORRESPONDENCE ADDRESS:

ADDRESSER: Sim & McBurney

STREET: 6th Floor, 330 University Avenue

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/074,658

FILING DATE: 08-MAY-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-795

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-074-658-37

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1233 TTAATTTTCATTCA 1248

Db 18 TTAATTTTCATTCA 3

RESULT 245

US-08-930-117-5

Sequence 5, Application US/08930117

Patent No. 6210879

GENERAL INFORMATION:

APPLICANT: MELONI, Rolando

APPLICANT: LAURENT, Claudine

APPLICANT: WALLEY, Jacques

TITLE OF INVENTION: METHOD FOR DIAGNOSING SCHIZOPHRENIA

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Road, Mailstop 3C43

CITY: Collegeville

STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,117
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/05264
FILING DATE: 03-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR96/00650
FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fehner Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: ST95028-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-930-117-5

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2Y 905 GTTCTCTCTTTATTC 920
DB 1 GTTCTCTCTTTATTC 16

RESULT 246
US-09-721-822A-112
; Sequence 112, Application US/09721822A
; Patent No. 6306606
; GENERAL INFORMATION:
; APPLICANT: Michael J. Weber
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF MP-1 EXPRESSION
; FILE REFERENCE: RTS-0142
; CURRENT APPLICATION NUMBER: US/09/721,822A
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 112
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-09-721-822A-112

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1353 CTGTGTGTGTGTCT 1368
DB 3 CTGTGTGTGTGTCT 18

RESULT 247
US-09-387-341-149/C
; Sequence 149, Application US/09387341
; Patent No. 6410323
; GENERAL INFORMATION:
; APPLICANT: Roberts, M. Luisa
; APPLICANT: Cowsett, Lex M.
; TITLE OF INVENTION: Antisense Modulation of Human Rho Family Gene
; FILE REFERENCE: ISPH-0404
; CURRENT APPLICATION NUMBER: US/09/387,341
; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: 09/156,424
; EARLIER FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 09/156,979
; EARLIER FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 09/156,807
; EARLIER FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 09/161,015
; EARLIER FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 149
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-387-341-149

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 827 CCTGGATTTTCTG 842
DB 18 CCTGGATTTTCTG 3

RESULT 248
US-08-745-485A-15
; Sequence 15, Application US/08745485A
; Patent No. 6440660
; GENERAL INFORMATION:
; APPLICANT: Barker, Jr., Robert H.
; Rapaport, Bliezer
; Zamecnik, Paul C.
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED REVERSAL OF
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,485A
; FILING DATE: 12-NO. 6440660-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/634,588
; FILING DATE: 18-APR-1996
; APPLICATION NUMBER: US 08/560,474
; FILING DATE: 17-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2047CIP (47508.253)
TELEPHONE: (617)526-6000
TELEFAX: (617)526-5000
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
S-08-745-485A-15

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 1259 AAATAATTTTCTAGTA 1274
|||||
b 2 AAATAATTTCTGTA 17

RESULT 249
S-08-745-485A-16/c
Sequence 16, Application US/08745485A
Patent No. 6440660
GENERAL INFORMATION:
APPLICANT: Barker, Jr., Robert H.
Rapoport, Eliezer
Zamecnik, Paul C.
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED REVERSAL OF
DRUG RESISTANCE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/745,485A
FILING DATE: 12-Nov-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/634,588
FILING DATE: 18-APR-1996
APPLICATION NUMBER: US 08/560,474
FILING DATE: 17-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2047CIP (47508.253)
TELEPHONE: (617)526-6000
TELEFAX: (617)526-5000
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-745-485A-16

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1259 AAATAATTTTCTAGTA 1274
|||||
Db 17 AAATAATTTCTGTA 2

RESULT 250
US-09-425-233-12/c
Sequence 12, Application US/09425233
Patent No. 6472200
GENERAL INFORMATION:
APPLICANT: EDUARDO MITRANI
TITLE OF INVENTION: A DEVICE AND METHOD FOR PERFORMING A
TITLE OF INVENTION: BIOLOGICAL MODIFICATION OF A FLUID
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows 98
SOFTWARE: Word for Windows version 6.0 converted to
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,233
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 325/68
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-425-233-12

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 496 GCCAGATGCATACAA 511
|||||
Db 18 GCCTGAGGCATACAA 3

RESULT 251
US-09-319-588C-35
Sequence 35, Application US/09319588C
Patent No. 6509018
GENERAL INFORMATION:

```
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE-INSERM
; APPLICANT: ASSISTANCE PUBLIQUE-HOPITAUX DE PARIS
; APPLICANT: INSTITUT PASTEUR
; APPLICANT: MAULIERE, Philippe
; APPLICANT: LOUSSERT-AJAKA, Ibtissam
; APPLICANT: SIMON, Francois
; APPLICANT: SARAGOSTI, Sentob
; APPLICANT: BARRE-SINOUSSE, Francoise
; TITLE OF INVENTION: NON-M NON-O HIV STRAINS, FRAGMENTS AND APPLICATIONS.
; FILE REFERENCE: 598US12
; CURRENT APPLICATION NUMBER: US/09/319,588C
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: FR96/15087
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 18
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-319-588C-35

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 410 TATCCAGGAATCAGTG 425
Db 3 TATCCAGGAATCAGAG 18

RESULT 252
US-09-319-588C-91
; Sequence 91, Application US/09319588C
; Patent No. 6509018
; GENERAL INFORMATION:
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE-INSERM
; APPLICANT: ASSISTANCE PUBLIQUE-HOPITAUX DE PARIS
; APPLICANT: INSTITUT PASTEUR
; APPLICANT: MAULIERE, Philippe
; APPLICANT: LOUSSERT-AJAKA, Ibtissam
; APPLICANT: SIMON, Francois
; APPLICANT: SARAGOSTI, Sentob
; APPLICANT: BARRE-SINOUSSE, Francoise
; TITLE OF INVENTION: NON-M NON-O HIV STRAINS, FRAGMENTS AND APPLICATIONS.
; FILE REFERENCE: 598US12
; CURRENT APPLICATION NUMBER: US/09/319,588C
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: FR96/15087
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91 (corresponds to YRT2-2 pool of Figure 1)
; LENGTH: 18
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-319-588C-91

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 410 TATCCAGGAATCAGTG 425
Db 3 TATCCAGGAATCAGAG 18

RESULT 253
US-09-422-978-5250/c
```

```
; Sequence 5250, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5250
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-22771 for SEQ 1316,
US-09-422-978-5250

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 820 TGGAAATCCTCGATT 835
Db 17 TGGAAAGCCTCGTTT 2

RESULT 254
US-09-422-978-6086
; Sequence 6086, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6086
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-8831 for SEQ 2152,
US-09-422-978-6086

Query Match 1.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1566 TTTTACTGTTCTGA 1581
Db 1 TGTTACTGTTCTGA 16
```

RESULT 255
S-09-468-265-20
Sequence 20, Application US/09468265
Patent No. 6379928
GENERAL INFORMATION:
APPLICANT: Berka, Randy M
APPLICANT: Cullen, Daniel
APPLICANT: Gray, Gregory L
APPLICANT: Hayenga, Kirk J
APPLICANT: Lewis, Virgil B
TITLE OF INVENTION: Heterologous Polypeptides Expressed in Filamentous Fungi, Process
TITLE OF INVENTION: Making Same and Vectors for Making Same
FILE REFERENCE: A-42909-5
CURRENT APPLICATION NUMBER: US/09/468,265
CURRENT FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 08/484,384
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/284,942
PRIOR FILING DATE: 1994-08-02
PRIOR APPLICATION NUMBER: 07/413,010
PRIOR FILING DATE: 1989-09-25
PRIOR APPLICATION NUMBER: 07/163,219
PRIOR FILING DATE: 1988-02-26
PRIOR APPLICATION NUMBER: 06/882,224
PRIOR FILING DATE: 1986-07-07
PRIOR APPLICATION NUMBER: 06/771,374
PRIOR FILING DATE: 1985-08-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent in version 3.1
SEQ ID NO 20
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide probes
S-09-468-265-20
Query Match 1.0%; Score 12.6; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
1271 AGTAAAGTACATTA 1285
|||:||||:|:
2 ARTAYAAATAYATHA 16
RESULT 256
S-08-646-789A-4/c
Sequence 4, Application US/08646789A
Patent No. 6022863
GENERAL INFORMATION:
APPLICANT: Peyman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSER: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,789A
FILING DATE: May 21, 1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-006
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-646-789A-79
Query Match 1.0%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1016 TTTCAGGTGTAAC 1029
|||||:
14 TTTCAGGTGAAACT 1

REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-006
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-646-789A-4
Query Match 1.0%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1016 TTTCAGGTGTAAC 1029
DB 14 TTTCAGGTGAAACT 1
RESULT 257
US-08-646-789A-79/c
Sequence 79, Application US/08646789A
Patent No. 6022863
GENERAL INFORMATION:
APPLICANT: Peyman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSER: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,789A
FILING DATE: May 21, 1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-006
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-646-789A-79

Query Match 1.0%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1016 TTTCAGGTGTAAC 1029
|||||:
14 TTTCAGGTGAAACT 1


```

RESULT 258
US-08-617-010C-14
; Sequence 14, Application US/08617010C
; Patent No. 6194144
; GENERAL INFORMATION:
; APPLICANT: Hubert K star
; TITLE OF INVENTION: DNA SEQUENCING BY MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037-9103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,010C
; FILING DATE: 18-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178,216
; FILING DATE: 06-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/001,323
; FILING DATE: 07-JAN-1993
; NAME: Seidman, Stephanie L
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8400
; TELEFAX: 619-587-5360
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-617-010C-14

Query Match 1.0%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 458 TCAACACTTCATGT 471
DB 1 TCAACACTGCATGT 14

RESULT 259
US-09-566-591-14
; Sequence 14, Application US/09566591
; Patent No. 6238871
; GENERAL INFORMATION:
; APPLICANT: Hubert Kuster
; TITLE OF INVENTION: DNA SEQUENCING BY MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037-9103
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/566,591
FILING DATE: 08-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/617,010
FILING DATE: 18-MAR-1996
APPLICATION NUMBER: 08/178,216
FILING DATE: 06-JAN-1994
APPLICATION NUMBER: 08/001,323
FILING DATE: 07-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2012B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8400
TELEFAX: 858-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SBQ ID NO: 14:
US-09-566-591-14

Query Match 1.0%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 458 TCAACACTTCATGT 471
DB 1 TCAACACTGCATGT 14

RESULT 260
US-09-054-832-37
; Sequence 37, Application US/09054832
; Patent No. 6312894
; GENERAL INFORMATION:
; APPLICANT: Meyer, Rich
; TITLE OF INVENTION: IMPROVED HYBRIDIZATION AND
; TITLE OF INVENTION: MISMATCH DISCRIMINATION USING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,832
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/415,370
; FILING DATE: 03-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brennan, Sean M

```

REGISTRATION NUMBER: 39,917
 REFERENCE/DOCKET NUMBER: 34469-20004.20
 TELEPHONE: 650-813-5600
 TELEFAX: 650-494-0792
 TELEX: 706141

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

3-09-054-832-37

Query Match 1.0%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1564 TTTTCTTACTGTTT 1577
 |||||
 1 TTTTCTTACTGTTT 14

RESULT 263

3-08-744-481A-24
 Sequence 24, Application US/08744481A
 Patent No. 6428955

GENERAL INFORMATION:

APPLICANT: K ster, Hubert
 TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
 NUMBER OF SEQUENCES: 55
 CORRESPONDENCE ADDRESS:

ADDRESSEE: HELLER EHRMAN WHITE & MCRAULIPPE
 STREET: 4250 Executive Square, Suite 700
 CITY: La Jolla
 STATE: California
 COUNTRY: USA

ZIP: 92037-9103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/744,481A

FILING DATE: No. 6428955ember 6, 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/617,256

FILING DATE: March 18, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 24736-2004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)450-8400

TELEFAX: (617)587-5360

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

-08-744-481A-24

Query Match 1.0%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

458 TCAACACTTCATGT 471
 |||||
 1 TCAACACTTCATGT 14

RESULT 262

US-09-640-953-37

Sequence 37, Application US/09640953

Patent No. 6492345

GENERAL INFORMATION:

APPLICANT: Meyer, Rich

TITLE OF INVENTION: IMPROVED HYBRIDIZATION AND

MISMATCH DISCRIMINATION USING OLIGONUCLEOTIDES

CONJUGATED TO MINOR GROOVE BINDERS

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/640,953

FILING DATE: 16-Aug-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/054,832

FILING DATE: 03-APR-1998

APPLICATION NUMBER: 08/415,370

FILING DATE: 03-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Brennan, Sean M

REGISTRATION NUMBER: 39,917

REFERENCE/DOCKET NUMBER: 34469-20004.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-813-5600

TELEFAX: 650-494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-640-953-37

Query Match 1.0%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.7e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1564 TTTTCTTACTGTTT 1577

|||||

1 TTTTCTTACTGTTT 14

RESULT 263

US-08-319-492B-160

Sequence 160, Application US/08319492B

Patent No. 5616488

GENERAL INFORMATION:

APPLICANT: Sullivan, Sean M.

APPLICANT: Draper, Kenneth G.

APPLICANT: McSwiggen, James

APPLICANT: Stinchcomb, Dan T.

TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES

TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS

TITLE OF INVENTION: OF IL-5

NUMBER OF SEQUENCES: 751

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

```

; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994
;
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
;
; INFORMATION FOR SEQ ID NO: 160:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-319-492B-160
;
; Query Match 1.0%; Score 12.4; DB 1; Length 15;
; Best Local Similarity 71.4%; Pred. No. 2.1e+02;
; Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1081 AAGAAATTGGAAAA 1094
; DB 2 AAGAAUUUGUAAA 15
;
; RESULT 264
; US-08-319-492B-161
; Sequence 161, Application US/08319492B
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggan, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0

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; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994
;
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
;
; INFORMATION FOR SEQ ID NO: 161:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-319-492B-161
;
; Query Match 1.0%; Score 12.4; DB 1; Length 15;
; Best Local Similarity 71.4%; Pred. No. 2.1e+02;
; Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1081 AAGAAATTGGAAAA 1094
; DB 1 AAGAAUUUGUAAA 14
;
; RESULT 265
; US-08-088-658-52/c
; Sequence 52, Application US/08088658
; Patent No. 5641625
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; APPLICANT: M llesgaard, Niels E.
; TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
; TITLE OF INVENTION: NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/088,658
; FILING DATE: 19930702
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/054,363
; FILING DATE: 26-APRIL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lucci, Joseph
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: 1SIS-1052

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

3-08-088-658-52

Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

458 TCACACTTCATGT 471
14 TCACACTTCATGT 1

RESULT 266
3-08-334-847-325/c
Sequence 325, Application US/08334847
Patent No. 5693532

GENERAL INFORMATION:
APPLICANT: McSwiggen, James
APPLICANT: Draper, Kenneth
APPLICANT: Pavco, Pam
APPLICANT: Woolf, Tod
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNCYIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,847
FILING DATE: No. 5693532ember 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 325:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

3-08-334-847-325
Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1453 ACTTGTTATTATG 1466
DB 15 ACTTGTTATTATG 2

RESULT 267

US-08-317-432A-4
Sequence 4, Application US/08317432A
Patent No. 5710028
GENERAL INFORMATION:
APPLICANT: Nurit Eyal and Nir Navot
TITLE OF INVENTION: A method of quick screening and
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
STREET: 2940 Birchtree lane
CITY: Silver Spring
STATE: Maryland
COUNTRY: United States of America
ZIP: 20906

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,432A
FILING DATE: 4-Oct-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/919,872
FILING DATE: 27-Jul-92
APPLICATION NUMBER: 08/084,505
FILING DATE: 1-Jul-93
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 128/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-317-432A-4
Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1438 TTCTGCTCGTTGA 1451
DB 2 TTCTGCTCGTTGA 15

RESULT 268

US-08-311-486C-193
Sequence 193, Application US/08311486C
Patent No. 5811300
GENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kevin Kisch
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF-
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,486C
FILING DATE: September 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-311-486C-193

two

Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 28.6%; Pred. No. 2.le+02;
Matches 4; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
QY 1043 ATTATTATGATT 1056
DB 1 AUAUUUUUUUUU 14

RESULT 269
US-08-311-486C-202
Sequence 202, Application US/08311486C
Patent No. 5811300
GENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kevin Kisich
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF-
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles

STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,486C
FILING DATE: September 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 202:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-311-486C-202

two

Query Match 1.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 28.6%; Pred. No. 2.le+02;
Matches 4; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
QY 1045 TATTATCTATTTA 1058
DB 1 UAUUUUUUUUUU 14

RESULT 270
US-08-311-486C-717
Sequence 717, Application US/08311486C
Patent No. 5811300
GENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kevin Kisich
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF-
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0

```

; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-217
;
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; Matches 5; Conservative 8; Mismatches 1; Indels 0; Gaps 0;
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; RESULT 272
; US-08-292-620A-511
; Sequence 511, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
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; CITY: Los Angeles
; STATE: California
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; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA: described below:
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; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.

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